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OM protein - protein search, using sw model

Run on: July 27, 2005, 03:27:05 ; Search time 43 Seconds

(without alignments)  
451.366 Million cell updates/sec

Title: US-09-502-176-2

Perfect score: 1540

Sequence: 1 VYLSECKTGNGKNGYGTMSK.....TNSQVMEYCKIPSCDSRV 260

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Issued Patents AA:\*  
1: /cgn2\_6/prodata/1/1aa/5A\_COMB.pep:\*  
2: /cgn2\_6/prodata/1/1aa/5B\_COMB.pep:\*  
3: /cgn2\_6/prodata/1/1aa/6A\_COMB.pep:\*  
4: /cgn2\_6/prodata/1/1aa/6B\_COMB.pep:\*  
5: /cgn2\_6/prodata/1/1aa/6C\_COMB.pep:\*  
6: /cgn2\_6/prodata/1/1aa/Backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1540	100.0	260	4	US-09-982-516-1
2	1535	99.7	339	1	US-08-248-629A-3
3	1535	99.7	339	1	US-08-451-932-3
4	1535	99.7	339	1	US-08-452-260-3
5	1535	99.7	339	1	US-08-326-785-3
6	1535	99.7	339	2	US-08-612-788-3
7	1535	99.7	339	2	US-08-605-598B-3
8	1535	99.7	339	2	US-08-429-743-3
9	1535	99.7	339	2	US-08-866-735-3
10	1535	99.7	339	3	US-09-066-028-3
11	1535	99.7	339	4	US-09-335-325-3
12	1535	99.7	339	5	PCT-US95-05107-3
13	1535	99.7	374	3	US-09-377-250-2
14	1535	99.7	375	3	US-09-377-250-2
15	1535	99.7	378	2	US-08-612-788-42
16	1535	99.7	378	3	US-09-066-028-42
17	1535	99.7	378	4	US-09-206-059-1
18	1535	99.7	378	4	US-09-335-325-42
19	1535	99.7	451	3	US-09-377-250-1
20	1535	99.7	452	3	US-09-377-250-4
21	1535	99.7	790	1	US-08-469-486-54
22	1535	99.7	790	2	US-08-469-658-54
23	1535	99.7	791	1	US-08-643-219-1
24	1535	99.7	791	2	US-09-131-995-1
25	1535	99.7	791	2	US-08-832-087B-1
26	1535	99.7	791	3	US-08-851-350-1
27	1535	99.7	791	3	US-09-132-154-1

28	1535	99.7	791	4	US-08-991-761A-6	Sequence 6, Appli
29	1535	99.7	791	4	US-08-924-287A-1	Sequence 1, Appli
30	1535	99.7	810	1	US-07-854-603-2	Sequence 2, Appli
31	1535	99.7	810	1	US-08-147-000B-29	Sequence 29, Appli
32	1535	99.7	810	3	US-09-086-514-1	Sequence 1, Appli
33	1535	99.7	810	3	US-09-192-012-5	Sequence 5, Appli
34	1535	99.7	810	4	US-09-403-736-1	Sequence 1, Appli
35	1535	99.7	810	4	US-09-701-265-1	Sequence 1, Appli
36	1535	99.7	814	4	US-08-750-711-1	Sequence 1, Appli
37	1532	99.5	713	4	US-09-949-016-9983	Sequence 9983, Ap
38	1531	99.4	369	4	US-09-701-265-2	Sequence 2, Appli
39	1531	99.4	810	6	5200340-8	Patent No. 5200340
40	1531	99.4	810	6	5200340-8	Patent No. 5200340
41	1511	98.1	352	2	US-08-612-788-40	Sequence 40, Appli
42	1511	98.1	352	3	US-09-066-028-40	Sequence 40, Appli
43	1511	98.1	352	4	US-09-335-325-40	Sequence 3, Appli
44	1505	97.7	254	4	US-09-701-265-3	Sequence 30, Appli
45	1486	96.5	250	2	US-08-612-788-30	

#### ALIGNMENTS

```
RESULT 1
US-09-982-516-1
; Sequence 1, Application US/09982516
; Patent No. 6723536
; GENERAL INFORMATION:
; APPLICANT: Madsen, John
; APPLICANT: Liang, Hong
; APPLICANT: Sim, Kim Lee
; APPLICANT: Zhou, Xinhua
; APPLICANT: Chang-Munrad, Amy
; APPLICANT: Boerner, Renee J.
; APPLICANT: Berner, Louise L.
; APPLICANT: Mistry, Piroz R.
; APPLICANT: Schrimsher, Jeffrey L.
; TITLE OF INVENTION: Method of Producing and Purifying Angiostatin Protein
; FILE REFERENCE: 05213-0562 43170-264313
; CURRENT APPLICATION NUMBER: US/09/982,516
; PRIOR FILING DATE: 2002-09-10
; PRIOR APPLICATION NUMBER: PCT/US00/32843
; PRIOR FILING DATE: 2000-12-04
; PRIOR APPLICATION NUMBER: US 60/168,919
; PRIOR FILING DATE: 1999-12-03
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 260
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-982-516-1
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Query Match 100.0%; Score 1540; DB 4; Length 260;  
Best Local Similarity 100.0%; Pred. No. 3.3e-139;  
Matches 260; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	VYLSECKTGNGKNGYGTMSKSTGKSTGSPHRRPSPATHPSEGLEENYCRNPDN	60
DB	1	VYLSECKTGNGKNGYGTMSKSTGKSTGSPHRRPSPATHPSEGLEENYCRNPDN	60
QY	61	DPOGPMCTTDPPEKRYDCDILCEBSCMCHSGENVDGKSKTMSGUECAMDSQSHAH	120
DB	61	DPOGPMCTTDPPEKRYDCDILCEBSCMCHSGENVDGKSKTMSGUECAMDSQSHAH	120
QY	121	GYIPSKFPNKLKKYCRNDRRLRPWCFTTDDNKWELCDIPRCTTTPPSGPTVQCLK	180
DB	121	GYIPSKFPNKLKKYCRNDRRLRPWCFTTDDNKWELCDIPRCTTTPPSGPTVQCLK	180
QY	181	GTGENTRGNAVTVSGTCHQMSAQTPHHTERTPENPCNLDENYCRNDGRRAPWCHT	240
DB	181	GTGENTRGNAVTVSGTCHQMSAQTPHHTERTPENPCNLDENYCRNDGRRAPWCHT	240

QY	241	TNSQVRWEYCKIPSCDSSPV	260
Db	241	TNSQVRWEYCKIPSCDSSPV	260

RESULT 2

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US-08-248-629A-3
Sequence 3, Application US/08248629A
Patent No. 5639725
GENERAL INFORMATION:
APPLICANT: Folkman, Judah
APPLICANT: O'Reilly, Michael
TITLE OF INVENTION: Angiostatin and Method of Use
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Jones & Askew
STREET: 191 Peachtree Street, 37th Floor
CITY: Atlanta
STATE: Georgia
COUNTRY: USA
ZIP: 30303-1769
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50
COMPUTER: Macintosh
OPERATING SYSTEM: 7.0
SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/248,629A
FILING DATE: 04/26/94
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Larry W. Stults, Ph.D.
REGISTRATION NUMBER: 34,025
REFERENCE/DOCKET NUMBER: 05213-0120
TELECOMMUNICATION INFORMATION:
TELEPHONE: 404-818-3700
TELEFAX: 404-818-3799
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 339
TYPE: amino acid
TOPOLOGY: linear
US-08-248-629A-3

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Query Match	99.7%	Score 1535	DB 1	Length 339
Best Local Similarity	99.6%	Pred. No. 1,4e-118		
Matches 259	Conservative	0	Mismatches 1	Indels 0
			Gaps	0
QY	1	VYLSEKTKNGKNYGTMSKTKNGITCCKMSTSPHPRPRSPATHPSEGLSEENYCNPN	60	
Db	1	VYLSEKTKNGKNYGTMSKTKNGITCCKMSTSPHPRPRSPATHPSEGLSEENYCNPN	60	
QY	61	DEQGPWCYTTDBEKRYDYCDLIECEECEMHSGSENYGKISKMSGLCECAMDSQPHH	120	
Db	61	DEQGPWCYTTDBEKRYDYCDLIECEECEMHSGSENYGKISKMSGLCECAMDSQPHH	120	
QY	121	GATPSPFPKKNLKNKYCNPNDBELAPWCFITTDVYNKRELCDIPRCTTPPPSSGPTYOCL	180	
Db	121	GATPSPFPKKNLKNKYCNPNDBELAPWCFITTDVYNKRELCDIPRCTTPPPSSGPTYOCL	180	
QY	181	GTGENYRGNAVAVTSGHCOHMSAQTPHTHERTEENPPCINLDENYCRNPDGGRAPWCHT	240	
Db	181	GTGENYRGNAVAVTSGHCOHMSAQTPHTHARTENPPCINLDENYCRNPDGGRAPWCHT	240	
QY	241	TNSOVRMEYCKIPSCDSSPV	260	
Db	241	TNSOVRMEYCKIPSCDSSPV	260	

RESULT 3  
US-08-451-932-3  
; Sequence 3, Application US/08451932  
; Patent No. 5733876

Query Match	99.7%;	Score 1535;	DB 1;	Length 339;
Best Local Similarity	99.6%;	Pred. 1.4e-138;		
Matches 259;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0
Qy	1	VYI <del>SE</del> CTGNGKNT <del>RG</del> MTSKTNGIT <del>Q</del> OKMS <del>ST</del> SPHPR <del>PS</del> PATH <del>PS</del> EGL <del>EN</del> T <del>CR</del> PN	60	
Db	1	VYI <del>SE</del> CTGNGKNT <del>RG</del> MTSKTNGIT <del>Q</del> OKMS <del>ST</del> SPHPR <del>PS</del> PATH <del>PS</del> EGL <del>EN</del> T <del>CR</del> PN	60	
Qy	61	D <del>P</del> Q <del>P</del> M <del>C</del> Y <del>T</del> T <del>D</del> E <del>P</del> K <del>R</del> Y <del>D</del> Y <del>C</del> DI <del>LE</del> CE <del>EC</del> EC <del>MC</del> SG <del>EN</del> Y <del>G</del> KI <del>S</del> K <del>T</del> MS <del>G</del> LE <del>C</del> Q <del>A</del> MD <del>S</del> Q <del>S</del> PH <del>A</del> H	120	
Db	61	D <del>P</del> Q <del>P</del> M <del>C</del> Y <del>T</del> T <del>D</del> E <del>P</del> K <del>R</del> Y <del>D</del> Y <del>C</del> DI <del>LE</del> CE <del>EC</del> EC <del>MC</del> SG <del>EN</del> Y <del>G</del> KI <del>S</del> K <del>T</del> MS <del>G</del> LE <del>C</del> Q <del>A</del> MD <del>S</del> Q <del>S</del> PH <del>A</del> H	120	
Qy	121	GIYI <del>S</del> K <del>P</del> PN <del>K</del> OL <del>K</del> KNY <del>CR</del> NP <del>D</del> REL <del>R</del> PM <del>C</del> FT <del>T</del> D <del>P</del> Y <del>K</del> RW <del>E</del> LC <del>D</del> I <del>P</del> RC <del>T</del> TP <del>P</del> SS <del>G</del> PT <del>Y</del> Q <del>C</del> L	180	
Db	121	GIYI <del>S</del> K <del>P</del> PN <del>K</del> OL <del>K</del> KNY <del>CR</del> NP <del>D</del> REL <del>R</del> PM <del>C</del> FT <del>T</del> D <del>P</del> Y <del>K</del> RW <del>E</del> LC <del>D</del> I <del>P</del> RC <del>T</del> TP <del>P</del> SS <del>G</del> PT <del>Y</del> Q <del>C</del> L	180	
Qy	181	GT <del>G</del> EN <del>Y</del> RG <del>N</del> VA <del>V</del> Y <del>S</del> GH <del>T</del> CO <del>H</del> MS <del>A</del> QT <del>P</del> HT <del>ER</del> P <del>EN</del> FP <del>C</del> K <del>U</del> L <del>D</del> EN <del>Y</del> CR <del>N</del> P <del>G</del> K <del>A</del> PM <del>C</del> HT	240	
Db	181	GT <del>G</del> EN <del>Y</del> RG <del>N</del> VA <del>V</del> Y <del>S</del> GH <del>T</del> CO <del>H</del> MS <del>A</del> QT <del>P</del> HT <del>ER</del> P <del>EN</del> FP <del>C</del> K <del>U</del> L <del>D</del> EN <del>Y</del> CR <del>N</del> P <del>G</del> K <del>A</del> PM <del>C</del> HT	240	
Qy	241	TNS <del>O</del> V <del>R</del> WE <del>Y</del> CKI <del>P</del> SC <del>D</del> SS <del>P</del> V	260	
Db	241	TNS <del>O</del> V <del>R</del> WE <del>Y</del> CKI <del>P</del> SC <del>D</del> SS <del>P</del> V	260	

RESULT 4  
US-08-453-260-3  
; Sequence 3, Application US/0845226C  
; Patent No. 5776704  
; GENERAL INFORMATION:

APPLICANT: Folkman, Judah  
TITLE OF INVENTION: Method of Diagnosing an Angiogenic  
TITLE OF INVENTION: Disease  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Jones & Askew  
STREET: 191 Peachtree Street, 37th Floor  
CITY: Atlanta  
STATE: Georgia  
COUNTRY: USA  
ZIP: 30303-1769  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50  
COMPUTER: Macintosh  
OPERATING SYSTEM: 7.0  
SOFTWARE: Microsoft Word  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/452,260  
FILING DATE: 05/26/95  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/248,629  
FILING DATE: 04/26/94  
ATTORNEY/AGENT INFORMATION:  
NAME: Larry W. Scults, Ph.D.  
REGISTRATION NUMBER: 34,025  
REFERENCE/DOCKET NUMBER: 05213-0124  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 404-818-3700  
TELEFAX: 404-818-3799  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 339  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-452-260-3

Query Match 99.7%; Score 1535; DB 1; Length 339;  
Best Local Similarity 99.6%; Pred. No. 1.4e-138;  
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VYLSECKTNGKNGKRGTMKTKNGITCOKWSSTSPHRRPSPATHPSEGLEENYCRNPDN 60  
DB 1 VYLSECKTNGKNGKRGTMKTKNGITCOKWSSTSPHRRPSPATHPSEGLEENYCRNPDN 60  
QY 61 DPOGWCCTTDPBKRYDYCDILECEBECMHGSGENYDGKISKTMSGLECOAWDSOPH 120  
DB 61 DPOGWCCTTDPBKRYDYCDILECEBECMHGSGENYDGKISKTMSGLECOAWDSOPH 120  
QY 121 GYIPSKFPKNLKKNYCRNPDRRLPWCFTTDPNKMELCDIPRCTTTPSSGPTYOCLK 180  
DB 121 GYIPSKFPKNLKKNYCRNPDRRLPWCFTTDPNKMELCDIPRCTTTPSSGPTYOCLK 180  
QY 181 GTGENYRGNAVAVTSGHTCOHWSAQTPTHTERTPENFPCKNLDENYCRNPDGKRAPWCHT 240  
DB 181 GTGENYRGNAVAVTSGHTCOHWSAQTPTHTERTPENFPCKNLDENYCRNPDGKRAPWCHT 240  
QY 241 TNSQVRWEYCKIPSCDSSPV 260  
DB 241 TNSQVRWEYCKIPSCDSSPV 260

RESULT 5  
US-08-326-785-3  
Sequence 3, Application US/08326785  
Patent No. 5792845  
GENERAL INFORMATION:  
APPLICANT: Folkman, Judah  
APPLICANT: O'Reilly, Michael  
TITLE OF INVENTION: Angiostatin and Method of Use  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:

ADDRESSEE: Jones & Askew  
STREET: 191 Peachtree Street, 37th Floor  
CITY: Atlanta  
STATE: Georgia  
COUNTRY: USA  
ZIP: 30303-1769  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50  
COMPUTER: Macintosh  
OPERATING SYSTEM: 7.0  
SOFTWARE: Microsoft Word  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/326,785  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/248,629  
FILING DATE: 04/26/94  
ATTORNEY/AGENT INFORMATION:  
NAME: Larry W. Scults, Ph.D.  
REGISTRATION NUMBER: 34,025  
REFERENCE/DOCKET NUMBER: 05213-0121  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 404-818-3700  
TELEFAX: 404-818-3799  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 339  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-326-785-3

Query Match 99.7%; Score 1535; DB 1; Length 339;  
Best Local Similarity 99.6%; Pred. No. 1.4e-138;  
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VYLSECKTNGKNGKRGTMKTKNGITCOKWSSTSPHRRPSPATHPSEGLEENYCRNPDN 60  
DB 1 VYLSECKTNGKNGKRGTMKTKNGITCOKWSSTSPHRRPSPATHPSEGLEENYCRNPDN 60  
QY 61 DPOGWCCTTDPBKRYDYCDILECEBECMHGSGENYDGKISKTMSGLECOAWDSOPH 120  
DB 61 DPOGWCCTTDPBKRYDYCDILECEBECMHGSGENYDGKISKTMSGLECOAWDSOPH 120  
QY 121 GYIPSKFPKNLKKNYCRNPDRRLPWCFTTDPNKMELCDIPRCTTTPSSGPTYOCLK 180  
DB 121 GYIPSKFPKNLKKNYCRNPDRRLPWCFTTDPNKMELCDIPRCTTTPSSGPTYOCLK 180  
QY 181 GTGENYRGNAVAVTSGHTCOHWSAQTPTHTERTPENFPCKNLDENYCRNPDGKRAPWCHT 240  
DB 181 GTGENYRGNAVAVTSGHTCOHWSAQTPTHTERTPENFPCKNLDENYCRNPDGKRAPWCHT 240  
QY 241 TNSQVRWEYCKIPSCDSSPV 260  
DB 241 TNSQVRWEYCKIPSCDSSPV 260

RESULT 6  
US-08-612-788-3  
Sequence 3, Application US/08612788  
Patent No. 5837682  
GENERAL INFORMATION:  
APPLICANT: Folkman, W. Judah  
APPLICANT: O'Reilly, Michael  
APPLICANT: Cao, Yihai  
APPLICANT: Sim, B. Kim Lee  
TITLE OF INVENTION: Angiostatin Fragments and Method of Use  
NUMBER OF SEQUENCES: 45  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Jones & Askew  
STREET: 191 Peachtree Street, 37th Floor  
CITY: Atlanta  
STATE: Georgia

COUNTRY: U.S.  
ZIP: 30303-1769  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/612,788  
FILING DATE:  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Warren, William L.  
REGISTRATION NUMBER: 36,714  
REFERENCE/DOCKET NUMBER: 05213-0126  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 404-818-3700  
TELEFAX: 404-818-3799  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 339 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: N-terminal  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
IMMEDIATE SOURCE:  
CLONE: Angiostatin fragment  
US-08-612-788-3

Query Match 99.7%; Score 1535; DB 2; Length 339;  
Best Local Similarity 99.6%; Pred. No. 1,4e-138;  
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VYLSECKTGNGKNGYRGMTSKNGITCQKWSSTSPRRPRSPATHPSEGLEENYCRNPDN 60  
DB 1 VYLSECKTGNGKNGYRGMTSKNGITCQKWSSTSPRRPRSPATHPSEGLEENYCRNPDN 60  
QY 61 DPGQWCYTTDPBKRKYDYCDILCEBECMHCSEGENYDGIKSTMSGLECOAMDSQSPHAA 120  
DB 61 DPGQWCYTTDPBKRKYDYCDILCEBECMHCSEGENYDGIKSTMSGLECOAMDSQSPHAA 120  
QY 121 GYIPSKFPNKNLKKNYCRNPDELRPMCFETDPNKRWELCDIPRCTTPPSSGPTYQCLK 180  
DB 121 GYIPSKFPNKNLKKNYCRNPDELRPMCFETDPNKRWELCDIPRCTTPPSSGPTYQCLK 180  
QY 181 GTGENYRGNAVAVTSGHTCOHMSAQTPTHTERTPENFPCKNLDENYCRNPDGGRAPWCHT 240  
DB 181 GTGENYRGNAVAVTSGHTCOHMSAQTPTHTERTPENFPCKNLDENYCRNPDGGRAPWCHT 240  
QY 241 TNSQVRWEYCKIPSCDSSPV 260  
DB 241 TNSQVRWEYCKIPSCDSSPV 260

RESULT 7  
US-08-605-598B-3  
Sequence 3, Application US/08605598B  
Patent No. 5861372  
GENERAL INFORMATION:  
APPLICANT: Folkman, M. Judah  
APPLICANT: Lin, Jie  
APPLICANT: O'Reilly, Michael S.  
TITLE OF INVENTION: Aggregating Angiostatin and Method of Use  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Jones & Askew  
STREET: 191 Peachtree Street, 37th Floor  
CITY: Atlanta

STATE: Georgia  
COUNTRY: U.S.  
ZIP: 30303-1769  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/605,598B  
FILING DATE: 22-FEB-1996  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Warren, William L.  
REGISTRATION NUMBER: 36,714  
REFERENCE/DOCKET NUMBER: 05213-0127  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 404-818-3700  
TELEFAX: 404-818-3799  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 339 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
ORIGINAL SOURCE:  
ORGANISM: Human Angiostatin  
US-08-605-598B-3

Query Match 99.7%; Score 1535; DB 2; Length 339;  
Best Local Similarity 99.6%; Pred. No. 1,4e-138;  
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VYLSECKTGNGKNGYRGMTSKNGITCQKWSSTSPRRPRSPATHPSEGLEENYCRNPDN 60  
DB 1 VYLSECKTGNGKNGYRGMTSKNGITCQKWSSTSPRRPRSPATHPSEGLEENYCRNPDN 60  
QY 61 DPGQWCYTTDPBKRKYDYCDILCEBECMHCSEGENYDGIKSTMSGLECOAMDSQSPHAA 120  
DB 61 DPGQWCYTTDPBKRKYDYCDILCEBECMHCSEGENYDGIKSTMSGLECOAMDSQSPHAA 120  
QY 121 GYIPSKFPNKNLKKNYCRNPDELRPMCFETDPNKRWELCDIPRCTTPPSSGPTYQCLK 180  
DB 121 GYIPSKFPNKNLKKNYCRNPDELRPMCFETDPNKRWELCDIPRCTTPPSSGPTYQCLK 180  
QY 181 GTGENYRGNAVAVTSGHTCOHMSAQTPTHTERTPENFPCKNLDENYCRNPDGGRAPWCHT 240  
DB 181 GTGENYRGNAVAVTSGHTCOHMSAQTPTHTERTPENFPCKNLDENYCRNPDGGRAPWCHT 240  
QY 241 TNSQVRWEYCKIPSCDSSPV 260  
DB 241 TNSQVRWEYCKIPSCDSSPV 260

RESULT 8  
US-08-429-743-3  
Sequence 3, Application US/08429743  
Patent No. 5885795  
GENERAL INFORMATION:  
APPLICANT: O'Reilly, Michael  
APPLICANT: Folkman, M. Judah  
APPLICANT: Sim, Kim Lee  
APPLICANT: Cao, Yihai  
TITLE OF INVENTION: Angiostatin and Method of Use  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Jones & Askew  
STREET: 191 Peachtree Street, 37th Floor  
CITY: Atlanta  
STATE: Georgia  
COUNTRY: U.S.  
ZIP: 30303-1769

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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/429,743
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/248,629
FILING DATE: 26-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/326,785
FILING DATE: 20-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Johnson, James D.
REGISTRATION NUMBER: 31,771
REFERENCE/DOCKET NUMBER: 05213-0122
TELECOMMUNICATION INFORMATION:
TELEPHONE: 404-818-3700
TELEFAX: 404-818-3799
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 339 amino acids
TYPE: amino acid
STRANDEDNESS:
MOLECULE TYPE: linear
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-08-429-743-3

Query Match      99.7%; Score 1535; DB 2; Length 339;
Best Local Similarity 99.6%; Pred. No.-1.4e-138;
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VYLSECKTGNGKNGYRGKMTSKNGITCQKMSSTSPHRRPSPATHPSEGLEENYCRNPDN 60
DB 1 VYLSECKTGNGKNGYRGKMTSKNGITCQKMSSTSPHRRPSPATHPSEGLEENYCRNPDN 60
QY 61 DPQPMWCYTTDPKRYDYCDILCEBECMHGSGENYDGKISKTMGSLGECQAMDSQSPHAA 120
DB 61 DPQPMWCYTTDPKRYDYCDILCEBECMHGSGENYDGKISKTMGSLGECQAMDSQSPHAA 120
QY 121 GYISKFPKPKNLKKYCRNPDRELPRWCFTTDPNKRWELCDIPRCTTPPSSSGPTTQCLK 180
DB 121 GYISKFPKPKNLKKYCRNPDRELPRWCFTTDPNKRWELCDIPRCTTPPSSSGPTTQCLK 180
QY 181 GTGENYRGNAVAVTSGHTCOHMSAQTPTHTERTPENPCKNLDENYCRNPDGKRAPWCHT 240
DB 181 GTGENYRGNAVAVTSGHTCOHMSAQTPTHTERTPENPCKNLDENYCRNPDGKRAPWCHT 240
QY 241 TNSQVRWEYCKIIPSCDSSPV 260
DB 241 TNSQVRWEYCKIIPSCDSSPV 260

RESULT 9
US-08-866-735-3
Sequence 3, Application US/08866735
Patent No. 5945403
GENERAL INFORMATION:
APPLICANT: Folkman, M. Judah
APPLICANT: O'Reilly, Michael
TITLE OF INVENTION: Angiostatin Fragments and Method of Use
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jones & Askew, LLP
STREET: 191 Peachtree Street, 37th Floor
CITY: Atlanta
STATE: Georgia
```

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COUNTRY: USA
ZIP: 30303-1769
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/866,735
FILING DATE: 30-MAY-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Warren, William L.
REGISTRATION NUMBER: 36,714
REFERENCE/DOCKET NUMBER: 05940-0129
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 818-3700
TELEFAX: (404) 818-3799
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 339 amino acids
TYPE: amino acid
STRANDEDNESS:
MOLECULE TYPE: linear
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: Angiostatin fragment
US-08-866-735-3

Query Match      99.7%; Score 1535; DB 2; Length 339;
Best Local Similarity 99.6%; Pred. No.-1.4e-138;
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VYLSECKTGNGKNGYRGKMTSKNGITCQKMSSTSPHRRPSPATHPSEGLEENYCRNPDN 60
DB 1 VYLSECKTGNGKNGYRGKMTSKNGITCQKMSSTSPHRRPSPATHPSEGLEENYCRNPDN 60
QY 61 DPQPMWCYTTDPKRYDYCDILCEBECMHGSGENYDGKISKTMGSLGECQAMDSQSPHAA 120
DB 61 DPQPMWCYTTDPKRYDYCDILCEBECMHGSGENYDGKISKTMGSLGECQAMDSQSPHAA 120
QY 121 GYISKFPKPKNLKKYCRNPDRELPRWCFTTDPNKRWELCDIPRCTTPPSSSGPTTQCLK 180
DB 121 GYISKFPKPKNLKKYCRNPDRELPRWCFTTDPNKRWELCDIPRCTTPPSSSGPTTQCLK 180
QY 181 GTGENYRGNAVAVTSGHTCOHMSAQTPTHTERTPENPCKNLDENYCRNPDGKRAPWCHT 240
DB 181 GTGENYRGNAVAVTSGHTCOHMSAQTPTHTERTPENPCKNLDENYCRNPDGKRAPWCHT 240
QY 241 TNSQVRWEYCKIIPSCDSSPV 260
DB 241 TNSQVRWEYCKIIPSCDSSPV 260

RESULT 10
US-09-066-028-3
Sequence 3, Application US/09066028
Patent No. 6024688
GENERAL INFORMATION:
APPLICANT: Folkman, M. Judah
APPLICANT: O'Reilly, Michael
APPLICANT: Cao, Yihai
APPLICANT: Sim, B. Kim Lee
TITLE OF INVENTION: Angiostatin Fragments and Method of Use
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jones & Askew
STREET: 191 Peachtree Street, 37th Floor
```

CITY: Atlanta  
STATE: Georgia  
COUNTRY: U.S.  
ZIP: 30303-1769  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/066,028  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/612,788  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Warren, William L.  
REGISTRATION NUMBER: 36,714  
REFERENCE/DOCKET NUMBER: 05213-0126  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 404-818-3700  
TELEFAX: 404-818-3799  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 339 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: N-terminal  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
IMMEDIATE SOURCE:  
CLONE: Angiostatin fragment  
US-09-066-028-3

Query Match 99.7%; Score 1535; DB 3; Length 339;  
Best Local Similarity 99.6%; Pred. No. 1,4e-138;  
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VYLSECKTGNGKNTKGTGKTKNGITCQKMSSTSPHRRFSPATHPSEGLEENYCRNPDN 60  
DB 1 VYLSECKTGNGKNTKGTGKTKNGITCQKMSSTSPHRRFSPATHPSEGLEENYCRNPDN 60  
QY 61 DPOGPMCTTTPDEKRYDYCDILECEBECMHCSGNGYDGIKSTMSGLECQAMDSQSPHAA 120  
DB 61 DPOGPMCTTTPDEKRYDYCDILECEBECMHCSGNGYDGIKSTMSGLECQAMDSQSPHAA 120  
QY 121 GYIPSKFPMKXKXKNCNPDRELPRWCFTTDPNKRWELCDIPRCTTPPPSSGPTVQCLK 180  
DB 121 GYIPSKFPMKXKXKNCNPDRELPRWCFTTDPNKRWELCDIPRCTTPPPSSGPTVQCLK 180  
QY 181 GTGNGYRGNAVAVTVSGHTCQHMSAQTPTHTERTPENFPCKNLDENYCRNPDGKRAFWCHT 240  
DB 181 GTGNGYRGNAVAVTVSGHTCQHMSAQTPTHTERTPENFPCKNLDENYCRNPDGKRAFWCHT 240  
QY 241 TNSQVMEYCKIIPSCDSSPV 260  
DB 241 TNSQVMEYCKIIPSCDSSPV 260

RESULT 11  
US-09-335-325-3  
Sequence 3, Application US/09335325  
Patent No. 652139  
GENERAL INFORMATION:  
APPLICANT: Folkman, M. Judah  
O'Reilly, Michael  
Cao, Yihai  
Sim, B. Kim Lee

TITLE OF INVENTION: Angiostatin Fragments and Method of Use  
NUMBER OF SEQUENCES: 45  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Jones & Askew  
STREET: 191 Peachtree Street, 37th Floor  
CITY: Atlanta  
STATE: Georgia  
COUNTRY: U.S.  
ZIP: 30303-1769  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/335,325  
FILING DATE: 17-Jun-1999  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/612,788  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Warren, William L.  
REGISTRATION NUMBER: 36,714  
REFERENCE/DOCKET NUMBER: 05213-0126  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 404-818-3700  
TELEFAX: 404-818-3799  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 339 amino acids  
TYPE: amino acid  
STRANDEDNESS: <Unknown>  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: N-terminal  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
IMMEDIATE SOURCE:  
CLONE: Angiostatin fragment  
SEQUENCE DESCRIPTION: SEQ ID NO: 3:  
US-09-335-325-3

Query Match 99.7%; Score 1535; DB 4; Length 339;  
Best Local Similarity 99.6%; Pred. No. 1,4e-138;  
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VYLSECKTGNGKNTKGTGKTKNGITCQKMSSTSPHRRFSPATHPSEGLEENYCRNPDN 60  
DB 1 VYLSECKTGNGKNTKGTGKTKNGITCQKMSSTSPHRRFSPATHPSEGLEENYCRNPDN 60  
QY 61 DPOGPMCTTTPDEKRYDYCDILECEBECMHCSGNGYDGIKSTMSGLECQAMDSQSPHAA 120  
DB 61 DPOGPMCTTTPDEKRYDYCDILECEBECMHCSGNGYDGIKSTMSGLECQAMDSQSPHAA 120  
QY 121 GYIPSKFPMKXKXKNCNPDRELPRWCFTTDPNKRWELCDIPRCTTPPPSSGPTVQCLK 180  
DB 121 GYIPSKFPMKXKXKNCNPDRELPRWCFTTDPNKRWELCDIPRCTTPPPSSGPTVQCLK 180  
QY 181 GTGNGYRGNAVAVTVSGHTCQHMSAQTPTHTERTPENFPCKNLDENYCRNPDGKRAFWCHT 240  
DB 181 GTGNGYRGNAVAVTVSGHTCQHMSAQTPTHTERTPENFPCKNLDENYCRNPDGKRAFWCHT 240  
QY 241 TNSQVMEYCKIIPSCDSSPV 260  
DB 241 TNSQVMEYCKIIPSCDSSPV 260

RESULT 12  
PCT-US95-05107-3  
Sequence 3, Application PC/TUS9505107

GENERAL INFORMATION:  
APPLICANT: THE CHILDREN'S MEDICAL CENTER, CORPORATION  
TITLE OF INVENTION: Angiostatin and Method of Use  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Jones & Akeaw  
STREET: 191 Peachtree Street, 37th Floor  
CITY: Atlanta  
STATE: Georgia  
COUNTRY: U.S.  
ZIP: 30303-1769  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/05107  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/248,629  
FILING DATE: 26-APR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/326,785  
FILING DATE: 20-OCT-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Johnson, James D.  
REGISTRATION NUMBER: 31,771  
REFERENCE/DOCKET NUMBER: 05213-0122  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 404-818-3700  
TELEFAX: 404-818-3799  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 339 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
PCT-US95-05107-3

Query Match 99.7%; Score 1535; DB 5; Length 339;  
Best Local Similarity 99.6%; Pred. No. 1.4e-138;  
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VYLSECKTGNGKNGYGTMSKTNGITCQKWSSTSPHPRPSPATHPSEGLEENYCRNPND 60  
DB 1 VYLSECKTGNGKNGYGTMSKTNGITCQKWSSTSPHPRPSPATHPSEGLEENYCRNPND 60  
QY 61 DPOGWCYTTDPKRYDYCDILECEECCHGSGENYDGIKSTMSGLECOAMDSPHAA 120  
DB 61 DPOGWCYTTDPKRYDYCDILECEECCHGSGENYDGIKSTMSGLECOAMDSPHAA 120  
QY 121 GIYPSKFPKNNLKKYCCRNPDRELRPWCFTTDPNKKWELCDIPRCTPPSSGPTYQCLK 180  
DB 121 GIYPSKFPKNNLKKYCCRNPDRELRPWCFTTDPNKKWELCDIPRCTPPSSGPTYQCLK 180  
QY 181 GTGENTRGNAVAATVSGHTCOHWSAOTPHHTERTPENPCNLDENYCRNPDGRAPWCHT 240  
DB 181 GTGENTRGNAVAATVSGHTCOHWSAOTPHHTERTPENPCNLDENYCRNPDGRAPWCHT 240  
QY 241 TNSQVRWEYCKIPSCDSSPV 260  
DB 241 TNSQVRWEYCKIPSCDSSPV 260

RESULT 13  
US-09-377-250-3  
; Sequence 3, Application US/09377250

Patent No. 6365364  
GENERAL INFORMATION:  
APPLICANT: MANN, KENNETH G.  
TITLE OF INVENTION: ANGIOGENESIS INHIBITORS AND USERS THEREOF  
FILE REFERENCE: 48409/360  
CURRENT APPLICATION NUMBER: US/09/377,250  
CURRENT FILING DATE: 1999-08-19  
NUMBER OF SEQ ID NOS: 5  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 3  
LENGTH: 374  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: angiogenesis inhibitor  
NAME/KEY: MOD RES  
LOCATION: (264)  
OTHER INFORMATION: Xaa = Gln or Glu  
US-09-377-250-3

Query Match 99.7%; Score 1535; DB 3; Length 374;  
Best Local Similarity 99.6%; Pred. No. 1.6e-138;  
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VYLSECKTGNGKNGYGTMSKTNGITCQKWSSTSPHPRPSPATHPSEGLEENYCRNPND 60  
DB 1 VYLSECKTGNGKNGYGTMSKTNGITCQKWSSTSPHPRPSPATHPSEGLEENYCRNPND 60  
QY 61 DPOGWCYTTDPKRYDYCDILECEECCHGSGENYDGIKSTMSGLECOAMDSPHAA 120  
DB 61 DPOGWCYTTDPKRYDYCDILECEECCHGSGENYDGIKSTMSGLECOAMDSPHAA 120  
QY 121 GIYPSKFPKNNLKKYCCRNPDRELRPWCFTTDPNKKWELCDIPRCTPPSSGPTYQCLK 180  
DB 121 GIYPSKFPKNNLKKYCCRNPDRELRPWCFTTDPNKKWELCDIPRCTPPSSGPTYQCLK 180  
QY 181 GTGENTRGNAVAATVSGHTCOHWSAOTPHHTERTPENPCNLDENYCRNPDGRAPWCHT 240  
DB 181 GTGENTRGNAVAATVSGHTCOHWSAOTPHHTERTPENPCNLDENYCRNPDGRAPWCHT 240  
QY 241 TNSQVRWEYCKIPSCDSSPV 260  
DB 241 TNSQVRWEYCKIPSCDSSPV 260

RESULT 14  
US-09-377-250-2  
; Sequence 2, Application US/09377250  
Patent No. 6365364  
GENERAL INFORMATION:  
APPLICANT: MANN, KENNETH G.  
TITLE OF INVENTION: ANGIOGENESIS INHIBITORS AND USERS THEREOF  
FILE REFERENCE: 48409/360  
CURRENT APPLICATION NUMBER: US/09/377,250  
CURRENT FILING DATE: 1999-08-19  
NUMBER OF SEQ ID NOS: 5  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 2  
LENGTH: 375  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: angiogenesis inhibitor  
NAME/KEY: MOD RES  
LOCATION: (265)  
OTHER INFORMATION: Xaa = Gln or Glu  
US-09-377-250-2

Query Match 99.7%; Score 1535; DB 3; Length 375;

Best Local Similarity 99.6%; Pred. No. 1.6e-138;  
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 VILSECKTGNGKRYRGTMSTKNGITCQKWSSTSPHPRPSPATHPSEGLEENYCRNPDN 60  
Db 2 VILSECKTGNGKRYRGTMSTKNGITCQKWSSTSPHPRPSPATHPSEGLEENYCRNPDN 61  
Qy 61 DPGPWCYTTDPKRYDYCDILECEECCHGCGENYDGIKSTMSGLBQAWDSQSPH 120  
Db 62 DPGPWCYTTDPKRYDYCDILECEECCHGCGENYDGIKSTMSGLBQAWDSQSPH 121  
Qy 121 GYIPSKFPNNKLNKRYCRNPDRELPRWCFTTDPNKRWECDIPRCTTTPSSGPTYQCL 180  
Db 122 GYIPSKFPNNKLNKRYCRNPDRELPRWCFTTDPNKRWECDIPRCTTTPSSGPTYQCL 181  
Qy 181 GTGENYRGNAVAVTSGHTCQHSAGTPHTERTPENPCKNIDENYCRNPDGRAPWCHT 240  
Db 182 GTGENYRGNAVAVTSGHTCQHSAGTPHTERTPENPCKNIDENYCRNPDGRAPWCHT 241  
Qy 241 TNSQVRWEYCKIPSCDSSPV 260  
Db 242 TNSQVRWEYCKIPSCDSSPV 261

## RESULT 15

US-08-612-788-42

Sequence 42, Application US/08612788

Patent No. 5637682

GENERAL INFORMATION:

APPLICANT: Folkman, M. Judah

APPLICANT: O'Reilly, Micheal

APPLICANT: Cao, Yihai

APPLICANT: Sim, B. Kim Lee

TITLE OF INVENTION: Angiostatin Fragments and Method of Use

NUMBER OF SEQUENCES: 45

CORRESPONDENCE ADDRESS:

ADDRESSEE: Jones &amp; Askew

STREET: 191 Peachtree Street, 37th Floor

CITY: Atlanta

STATE: Georgia

COUNTRY: U.S.

ZIP: 30303-1769

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/612,788

FILING DATE:

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: Warren, William L.

REGISTRATION NUMBER: 36,714

REFERENCE/DOCKET NUMBER: 05213-0126

TELECOMMUNICATION INFORMATION:

TELEPHONE: 404-818-3700

TELEFAX: 404-818-3799

INFORMATION FOR SEQ ID NO: 42:

SEQUENCE CHARACTERISTICS:

LENGTH: 378 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

MOLECULE TYPE: protein

HYPOTHEetical: NO

ANTI-SENSE: NO

FRAGMENT TYPE: N-terminal

ORIGINAL SOURCE:

ORGANISM: Homo sapiens

IMMEDIATE SOURCE:

CLONE: K1-4BKL5

Query Match 99.7%; Score 1535; DB 2; Length 378;  
Best Local Similarity 99.6%; Pred. No. 1.6e-138;  
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 VILSECKTGNGKRYRGTMSTKNGITCQKWSSTSPHPRPSPATHPSEGLEENYCRNPDN 60  
Db 6 VILSECKTGNGKRYRGTMSTKNGITCQKWSSTSPHPRPSPATHPSEGLEENYCRNPDN 65  
Qy 61 DPGPWCYTTDPKRYDYCDILECEECCHGCGENYDGIKSTMSGLBQAWDSQSPH 120  
Db 66 DPGPWCYTTDPKRYDYCDILECEECCHGCGENYDGIKSTMSGLBQAWDSQSPH 125  
Qy 121 GYIPSKFPNNKLNKRYCRNPDRELPRWCFTTDPNKRWECDIPRCTTTPSSGPTYQCL 180  
Db 126 GYIPSKFPNNKLNKRYCRNPDRELPRWCFTTDPNKRWECDIPRCTTTPSSGPTYQCL 185  
Qy 181 GTGENYRGNAVAVTSGHTCQHSAGTPHTERTPENPCKNIDENYCRNPDGRAPWCHT 240  
Db 186 GTGENYRGNAVAVTSGHTCQHSAGTPHTERTPENPCKNIDENYCRNPDGRAPWCHT 245  
Qy 241 TNSQVRWEYCKIPSCDSSPV 260  
Db 246 TNSQVRWEYCKIPSCDSSPV 265

Search completed: July 27, 2005, 03:31:19  
Job time: 45 secs



Run on: July 27, 2005, 03:18:29 ; Search time 73 Seconds

1377.503 Million cell updates/sec

Title: US-09-502-176-2  
 Page: 1540

Sequence: 1 VYLSECKTGNGKNYRGTMSK.....TNSQVRWEYCKIPSCDSSPV 260

Scoring table: BLOSUM62

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

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Minimum DB seq length: 0
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Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*

1: geneseqp1980s: \*  
2: geneseqp1990s: \*  
3: geneseqp2000s: \*  
4: geneseqp2001s: \*  
5: geneseqp2002s: \*  
6: geneseqp2003as: \*  
7: geneseqp2003bs: \*  
8: geneseqp2004s: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1540	100.0	260	3	AAB26486	AAB26486 Deglycosylated
2	1540	100.0	260	4	AAU01209	AAU01209 Human ang
3	1537	99.8	869	7	ADK40316	ADK40316 C-termin
4	1537	99.8	869	7	ADK40314	ADK40314 N-termin
5	1535	99.7	260	6	AAI79748	AAI79748 Human p14
6	1535	99.7	268	2	AAI02109	AAI02109 A multipe
7	1535	99.7	285	2	AAI02102	AAI02102 A multipe
8	1535	99.7	339	2	AAR83961	AAR83961 Human p14
9	1535	99.7	339	2	AAW07581	AAW07581 N-Termina
10	1535	99.7	339	2	AAW94038	AAW94038 Human ang
11	1535	99.7	339	7	AAAM5018	AAAM5018 Human ang
12	1535	99.7	339	7	ADG47024	ADG47024 Human ang
13	1535	99.7	339	8	ADMI1543	ADMI1543 Human p14
14	1535	99.7	363	3	AAI70255	AAI70255 Human ang
15	1535	99.7	364	2	AAI02106	AAI02106 A multipe
16	1535	99.7	375	3	AAI79226	AAI79226 Angiogen
17	1535	99.7	375	3	AAI79225	AAI79225 Angiogen
18	1535	99.7	378	2	AAW07579	AAW07579 Human k
19	1535	99.7	378	3	AAI16450	AAI16450 Human ang
20	1535	99.7	378	5	AAAM4894	AAAM4894 Human ang
21	1535	99.7	378	7	ADG47063	ADG47063 Human k
22	1535	99.7	380	2	AAI02105	AAI02105 A multipe
23	1535	99.7	381	2	AAI02101	AAI02101 A multipe
24	1535	99.7	391	6	ADA08454	ADA08454 Mammalian
25	1535	99.7	391	8	ADP67426	ADP67426 A61 anti-

26	1535	99.7	394	6	ADA08455	Ada08455	Mammalia
27	1535	99.7	394	6	ADP67427	Adp67427	Acti anti-
28	1535	99.7	452	3	AA792224	Aa79224	Angiogen
29	1535	99.7	453	2	AA702093	Aa702093	A multi fu
30	1535	99.7	453	2	AA702099	Aa702099	A multi fu
31	1535	99.7	453	2	AA702095	Aa702095	A multi fu
32	1535	99.7	453	2	AA702096	Aa702096	A multi fu
33	1535	99.7	453	2	AAW95051	AaW95051	A multi fu
34	1535	99.7	470	2	AA702112	Aa702112	A multi fu
35	1535	99.7	480	7	ABU64288	Abu64288	Human ang
36	1535	99.7	484	6	ABA79749	AbA79749	Human pla
37	1535	99.7	563	5	ABB75942	Abb75942	Endothei
38	1535	99.7	566	2	AA702100	Aa702100	A multi fu
39	1535	99.7	571	5	ABB75944	Abb75944	Angiotens
40	1535	99.7	576	5	ABB75943	Abb75943	Angiotens
41	1535	99.7	579	8	ADG85312	Adg85312	Proactin
42	1535	99.7	654	8	ABM83810	Abm83810	Human dia
43	1535	99.7	672	8	ABM83809	Abm83809	Human dia
44	1535	99.7	714	7	ABG75025	Abg75025	Lys-plas
45	1535	99.7	790	2	AAR60519	Aar60519	Human 'G1

## ALIGNMENTS

XX	RESULT 1	
XX	AAAB26486	
ID	AAAB26486	standard; protein; 260 AA.
XX		
AC	AAAB26486;	
XX		
DT	16-JAN-2001	(first entry)
XX		
DE	Deglycosylated kringle 1-5 region protein.	
XX		
KM	Deglycosylated; kringle; angiogenesis; human.	
XX		
OS	Homo sapiens.	
XX		
PN	WO2000047729-A1.	
XX		
PD	17-AUG-2000.	
XX		
PF	10-FEB-2000; 2000WO-US003482.	
XX		
PR	10-FEB-1999; 99US-0119562P.	
PR	07-APR-1999; 99US-0128062P.	
XX		
PA	(ENTER-) ENTREMED INC.	
PA	(CHIL-) CHILDRENS MEDICAL CENT.	
XX		
PI	Pirie-Shepherd S, Folkman MJ, Liang H, Macdonald NJ, Sim KL;	
DR	WFI; 2000-579032/54.	
DR	N-PSDB; AAA94906.	
XX		
PT	Novel composition comprising deglycosylated fragments of kringle 1-5 regions of plasminogen linked to the glycosylated form, useful for inhibiting angiogenesis.	
XX		
PS	Claim 7; Fig 1; 42pp; English.	
XX		
CC	The present sequence is, deglycosylated kringle 1-5 region protein.	
CC	Deglycosylated kringle 1-5 region protein has increased antiangiogenic activity as compared to glycosylated kringle 1-5 region protein. The deglycosylated kringle 1-5 region protein was isolated from human plasminogen by affinity chromatography	
CC		
XX		
SO	Sequence 260 AA;	
XX		
Query Match	100.0%;	Score 1540; DB 3; Length 260;
Best Local Similarity	100.0%;	Pred. No. 8, 7e-91;
Matches 260; Conservative	0;	Mismatches 0;
Indels	0;	Gaps 0;

[illegible]

RESULT 2	
AAU01209	
ID	AAU01209 standard; protein; 260 AA.
XX	
AC	AAU01209;
XX	
DT	26-SEP-2001 (first entry)
XX	
DE	Human Angiotensin (hASv3) protein.
XX	
KW	Human; Angiotensin; recombinant production; cation exchange column;
KW	fermentation; angiogenesis mediated disease; leukaemia; tumour;
KW	rheumatoid arthritis; plaque neovascularisation.
XX	
OS	Homo sapiens.
XX	
PN	WC2001.40260-A2.
XX	
PD	07-JUN-2001.
XX	
PF	04-DEC-2000; 2000MO-US032843.
XX	
PR	03-DEC-1999; 99US-0168919P.
XX	
PA	(ENTR-) ENTREMED INC.
PI	Madсен J, Liang H, Sim KL, Zhou X, Chang-Murad A, Boerner RJ;
PI	Bermelo LL, Mistry FR, Schrimsher JL, Shepard SR;
DR	WPI; 2001-408277/43.
XX	
PT	Purifying recombinant angiotensin, involves applying fermented broth
PT	containing angiotensin to expanded bed cation exchange column, anion
PT	exchange column, hydroxyapatite column, hydrophobic column and a
PT	membrane.
XX	
PS	Example 1; Page 22; 49pp; English.
XX	
CC	The present sequence representing Angiotensin protein is given in an
CC	invention providing a method for recombinant production, recovery and
CC	purification of Angiotensin protein. Purification of recombinant
CC	Angiotensin comprises applying crude fermentation broth containing the
CC	protein to an expanded bed cation exchange column, eluting it, and
CC	applying the eluate to anion exchange column, repeating the process of
CC	eluting and applying, to hydroxyapatite column, hydrophobic column and
CC	membrane, in order, and collecting fluid passing through the membrane.
CC	Angiotensin is useful for treating angiogenesis mediated diseases,
CC	including solid tumours, leukaemia, tumour metastases, benign tumours,
CC	rheumatoid arthritis, psoriasis, ocular angiogenic diseases, Oler-Webber
CC	syndrome, myocardial angiogenesis plaque neovascularisation,

CC telangiectasia, haemophilic joints, angiodiroma and wound granulation.  
CC As a centrifugation technique is not employed in the process, damage to  
CC the cells with concomitant release of undesirable biological materials  
CC such as cytochromes, pigments, enzymes, chemicals and other undesirable  
CC cellular constituents and debris, is prevented. Large scale recovery and  
CC purification of proteins is greater than that obtained from prior art  
CC methods. Active Angiotensin can be stored in buffers for extended periods  
CC of time, in vials or other containers, either in solution which may be  
CC liquid or frozen, or lyophilised  
XX  
SQ Sequence 260 AA;

Query Match	100.0%;	Score 1540;	DB 4;	Length 260;
Best Local Similarity	100.0%;	Pred. No. 8.7e-91;		
Matches 260; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0

Qy	1	YLSECKKNGKNGNYGTMSTKTKNGITGCKMKSSTPHRPRFSPATHPBEGLEENYCNPN	60
Db	1	YLSECKKNGKNGNYGTMSTKTKNGITGCKMKSSTPHRPRFSPATHPBEGLEENYCNPN	60
Qy	61	DPQGPWCYTTDBEKKRYDCILICEEBECMHCSGENYDGKISKTMASGLECAMDSOPHAH	120
Db	61	DPQGPWCYTTDBEKKRYDCILICEEBECMHCSGENYDGKISKTMASGLECAMDSOPHAH	120
Qy	121	GYPSPKFPKXNLKKXKNCNPNRELRLPNCFTTDPKRMELCDIPRCTPPPSQPTQCLK	180
Db	121	GYPSPKFPKXNLKKXKNCNPNRELRLPNCFTTDPKRMELCDIPRCTPPPSQPTQCLK	180
Qy	181	GTGENYKGNVAVTYSGHTCQMSAQTPHTHERTEPNPCNLDBENYCRNPDGRAPWCHT	240
Db	181	GTGENYKGNVAVTYSGHTCQMSAQTPHTHERTEPNPCNLDBENYCRNPDGRAPWCHT	240
Qy	241	TNSQVRMEYCKIPSCDSSPV 260	
Db	241	TNSQVRMEYCKIPSCDSSPV 260	

RESULT 3
ID ADK40316
ADK40316 standard; protein; 869 AA.
XX AC ADK40316;
XX DT 06-MAY-2004 (first entry)
XX DE C-terminal albumin-angiotensin fusion protein.
XX KW cytostatic; vaccine; albumin fusion protein; KW angiogenesis inhibiting peptide; angiogenesis-dependent tumor; cancer; collagen.
XX OS Homo sapiens.
XX OS Synthetic.
XX PN WO2003066085-A1.
XX PD 14-AUG-2003.
XX PF 07-FEB-2003; 2003WO-IB000433.
XX PR 07-FEB-2002; 2002US-0355547P.
XX PA (AVET ) AVENTIS BEHRING GMBH. PA (DELZ ) DELTA BIOTECHNOLOGY LTD.
XX PT Martins P, Celik I, Kisker O, Sleep D, Hay J, Hauser H, PT and an albumin having an albumin activity, or their fragments or PT variants, useful for treating angiogenesis-dependent tumor, e.g. cancer.
XX DR WPI; 2003-731479/69.
XX DR N-PADB; ADK40315.

XX Disclosure; Fig 8; 136bp; English.  
PS  
XX  
CC The invention relates to an albumin fusion protein comprising an  
CC angiogenesis inhibiting peptide and an albumin having an albumin  
CC activity, or their fragments or variants. The albumin fusion proteins,  
CC compositions, vaccines and methods are useful for treating angiogenesis-  
CC dependent tumor, e.g. cancer. This sequence represents an C-terminal  
CC albumin-angiotensin fusion protein.  
SQ  
Sequence 869 AA;  
Query Match 99.8%; Score 1537; DB 7; Length 869;  
Best Local Similarity 99.6%; Pred. No. 4.2e-90;  
Matches 259; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 VYLSECKTGKNGKRGKMGSKTKNGITCQKWSSTSPHRPRSPATHPSEGLEENYCRNPDN 60  
DB 610 VYLSECKTGKNGKRGKMGSKTKNGITCQKWSSTSPHRPRSPATHPSEGLEENYCRNPDN 669  
QY 61 DPGPWCYTTDPEKRYDYCDILCEBECMHCSENGYDGIKSKTMSGLECQAMDSQSPH 120  
DB 670 DPGPWCYTTDPEKRYDYCDILCEBECMHCSENGYDGIKSKTMSGLECQAMDSQSPH 729  
QY 121 GYISKFPNNKLNKKNYCRNPDRELRPWCFTTDPNKKMELCDIPRCTPPSSGFTYQCL 180  
DB 730 GYISKFPNNKLNKKNYCRNPDRELRPWCFTTDPNKKMELCDIPRCTPPSSGFTYQCL 789  
QY 181 GTGENYGNVAVTSGHTCQWSAQTPTHTERTPENPCKNLDENYCRNPDGKRAPWCHT 240  
DB 790 GTGENYGNVAVTSGHTCQWSAQTPTHTERTPENPCKNLDENYCRNPDGKRAPWCHT 849  
QY 241 TNSQVRWEYCKIPSCDSSPV 260  
DB 850 TNSQVRWEYCKIPSCDSSPV 869  
RESULT 4  
ADK40314  
ID ADK40314 standard; protein; 869 AA.  
AC ADK40314;  
XX  
XX  
DT 06-MAY-2004 (first entry)  
XX  
XX N-terminal angiotensin-albumin fusion protein.  
XX  
XX cytosolic; vaccine; albumin fusion protein;  
XX  
XX angiogenesis inhibiting peptide; angiogenesis-dependent tumor; cancer;  
XX  
XX collagen.  
OS Homo sapiens.  
OS Synthetic.  
XX  
XX WO2003066085-A1.  
XX  
XX PD 14-AUG-2003.  
XX  
XX PF 07-FEB-2003; 2003WO-IB000433.  
XX  
XX PR 07-FEB-2002; 2002US-0355547P.  
XX  
XX PA (AVET) AVENTIS BEHRING GMBH.  
XX  
XX PA (DELTA) DELTA BIOTECHNOLOGY LTD.  
XX  
XX PI Mertine P, Celik I, Kisker O, Sleep D, Hay J, Hauser H;  
XX  
XX DR MPI: 2003-731479/69.  
XX  
XX DR N-PSDB; ADK40313.  
XX  
XX PT New albumin fusion protein comprising an angiogenesis inhibiting peptide  
XX  
XX PT and an albumin having an albumin activity, or their fragments or  
XX  
XX PT variants, useful for treating angiogenesis-dependent tumor, e.g. cancer.

XX  
PS Disclosure; Fig 6; 136bp; English.  
XX  
XX  
CC The invention relates to an albumin fusion protein comprising an  
CC angiogenesis inhibiting peptide and an albumin having an albumin  
CC activity, or their fragments or variants. The albumin fusion proteins,  
CC compositions, vaccines and methods are useful for treating angiogenesis-  
CC dependent tumor, e.g. cancer. This sequence represents an N-terminal  
CC angiotensin-albumin fusion protein.  
SQ  
Sequence 869 AA;  
Query Match 99.8%; Score 1537; DB 7; Length 869;  
Best Local Similarity 99.6%; Pred. No. 4.2e-90;  
Matches 259; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 VYLSECKTGKNGKRGKMGSKTKNGITCQKWSSTSPHRPRSPATHPSEGLEENYCRNPDN 60  
DB 25 VYLSECKTGKNGKRGKMGSKTKNGITCQKWSSTSPHRPRSPATHPSEGLEENYCRNPDN 84  
QY 61 DPGPWCYTTDPEKRYDYCDILCEBECMHCSENGYDGIKSKTMSGLECQAMDSQSPH 120  
DB 85 DPGPWCYTTDPEKRYDYCDILCEBECMHCSENGYDGIKSKTMSGLECQAMDSQSPH 144  
QY 121 GYISKFPNNKLNKKNYCRNPDRELRPWCFTTDPNKKMELCDIPRCTPPSSGFTYQCL 180  
DB 145 GYISKFPNNKLNKKNYCRNPDRELRPWCFTTDPNKKMELCDIPRCTPPSSGFTYQCL 204  
QY 181 GTGENYGNVAVTSGHTCQWSAQTPTHTERTPENPCKNLDENYCRNPDGKRAPWCHT 240  
DB 205 GTGENYGNVAVTSGHTCQWSAQTPTHTERTPENPCKNLDENYCRNPDGKRAPWCHT 264  
QY 241 TNSQVRWEYCKIPSCDSSPV 260  
DB 265 TNSQVRWEYCKIPSCDSSPV 284  
RESULT 5  
AAG79748  
ID AAG79748 standard; protein; 260 AA.  
AC AAG79748;  
XX  
XX  
XX  
DT 18-MAR-2003 (first entry)  
XX  
XX  
XX Human plasminogen kringle domains 1-3, Kl-3.  
XX  
XX  
XX Human; plasminogen; angiotensin; neovascularisation; kringle domain;  
XX  
XX cell proliferation; viral vector; replication-defective; cancer; tumour.  
XX  
XX  
XX Homo sapiens.  
XX  
XX OS  
XX WO200288173-A2.  
XX  
XX PD 07-NOV-2002.  
XX  
XX PF 29-APR-2002; 2002WO-US013461.  
XX  
XX PR 30-APR-2001; 2001US-0287673P.  
XX  
XX PR 05-APR-2002; 2002US-0370634P.  
XX  
XX PA (CELL-) CELL GENESYS INC.  
XX  
XX PI Chang B, Wu WW, MacArthur J, Patel S, Joos K, Mendez M;  
XX  
XX DR MPI: 2003-129131/12.  
XX  
XX DR N-PSDB; ABA00776.  
XX  
XX PT New recombinant viral vector expressing human angiotensin useful for  
XX  
XX PT inhibiting angiogenesis in a mammalian subject with cancer or tumor.  
XX  
XX PS Disclosure; Page 75-76; 83pp; English.





```

XX XX WO9635774-A2.
FN XX
PD XX 14-NOV-1996.
XX XX
PF XX 26-APR-1996; 96WO-US005856.
XX XX
PR 26-APR-1995; 95US-00429743.
PR 22-FEB-1996; 96US-00605598.
XX 08-MAR-1996; 96US-00612788.
PA (CHIL-) CHILDRENS MEDICAL CENT.
PI Folkman MJ, O'Reilly MS, Cao Y, Sim KL, Lin J;
PI WPI; 1996-518662/51.
XX
XX Use of angiotastatin fragments or aggregates - for inhibiting endothelial
PT cell proliferation and treating angiogenesis-mediated diseases, e.g.
PT cancer, arthritis or diabetic retinopathy.
XX
XX Claim 59; Page 96-97; 203pp; English.
XX
CC The invention relates to new methods and compositions for inhibiting
CC endothelial cell proliferation, using as active component an angiotastatin
CC fragment, a combination of angiotastatin fragments, or aggregate
CC angiotastatin. The fragment is preferably derived from murine, human,
CC Rhesus, porcine or bovine plasminogen and is a kringle 1, kringle 2,
CC kringle 3, kringle 2-3, kringle 1-3, kringle 1-2, kringle 1-4 or kringle
CC 1-4BKS protein. The aggregate angiotastatin has a Mol. Wt. of 45-65 kD and
CC is derived from a plasminogen fragment beginning at approximately amino
CC acid number 98 of murine, human, Rhesus, porcine or bovine plasminogen.
CC The active component can be used for treating angiogenesis-mediated
CC diseases such as cancer, arthritis, macular degeneration and diabetic
CC retinopathy. It can also be used to develop antibodies for use in
CC diagnosis, detection and therapy. The present sequence, which is the N-
CC terminal fragment of human angiotastatin, is a specific aggregate
CC angiotastatin which can be used in the invention
XX
SQ Sequence 339 AA:
Query Match 99.7%; Score 1535; DB 2; Length 339;
Best Local Similarity 99.6%; Pred. No. 2.3e-90;
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 VYLSECKTGNKNGKRYGTMSTKNGITCOKWSTSPHRRPSPATHPSEGLEENYCRNPN 60
Db 1 VYLSECKTGNKNGKRYGTMSTKNGITCOKWSTSPHRRPSPATHPSEGLEENYCRNPN 60
QY 61 DPOGFWCYTTDPEKRYDYCDILECEECMHCSENYDGKISKTWGSLGECQAWDSOSPFAH 120
Db 61 DPOGFWCYTTDPEKRYDYCDILECEECMHCSENYDGKISKTWGSLGECQAWDSOSPFAH 120
QY 121 GYIPSPKPNKLNKKNYCRNPNDRPWCFTTDPNKRKELCDIPRCTTTPSSGGTYQCLK 180
Db 121 GYIPSPKPNKLNKKNYCRNPNDRPWCFTTDPNKRKELCDIPRCTTTPSSGGTYQCLK 180
QY 181 GTEBNVAGNAVYVSGHTCOHWSAQTPHTERTPEENPCNLDENYCRNPDGKRAPCWCHT 240
Db 181 GTEBNVAGNAVYVSGHTCOHWSAQTPHTERTPEENPCNLDENYCRNPDGKRAPCWCHT 240
QY 241 TNSQVREWEYCKIPSCDSSPV 260
Db 241 TNSQVREWEYCKIPSCDSSPV 260
RESULT 10
ID AAW94038 standard; protein; 339 AA.
XX
XX AAW94038;
AC
XX
DT 06-APR-1999 (first entry)

```

```

XX XX Human angiotastatin fragment.
DE
XX
XX Plasminogen; kringle; endothelial; angiogenesis; tumour; leukaemia;
KW rheumatoid arthritis; psoriasis; ocular angiogenic disease; ulcer;
KW gene therapy; birth control; Crohn's disease; angiotastatin.
XX
XX Homo sapiens.
OS
XX
XX Key
FH Location/Qualifiers
FT Peptide 6..255
FT /note= "Kringle 1-3"
FT Peptide 6..165
FT /note= "Kringle 1-2"
FT Peptide 6..84
FT /note= "Kringle 1"
FT Peptide 86..255
FT /note= "Kringle 2-3"
FT Peptide 88..165
FT /note= "Kringle 2"
FT Peptide 178..255
FT /note= "Kringle 3"
XX
XX WO9854217-A1.
XX
XX 03-DEC-1998.
XX
XX 29-MAY-1998; 98WO-US010979.
XX
XX 30-MAY-1997; 97US-00866735.
XX
XX (CHIL-) CHILDRENS MEDICAL CENT.
XX
XX Folkman MJ, O'Reilly MS;
XX WPI; 1999-059809/05.
XX
XX Use of plasminogen fragments - having an amino acid sequence similar to
PT the kringle 1-5 region, for inhibiting endothelial cell proliferation and
PT angiogenesis.
XX
XX Example 27; Fig 2A-C; 165pp; English.
XX
XX The invention relates to inhibition of endothelial cell proliferation
CC that comprises administering to an endothelial cell a plasminogen
CC fragment having an amino acid sequence similar to the kringle 1-5 region
CC of a plasminogen molecule. The plasminogen fragments can be derived from
CC murine, human, Rhesus, porcine or bovine plasminogens. The plasminogen
CC fragments can be used for modulating angiogenesis and treating angiogenic
CC mediated disease e.g. solid tumours; for treating excessive or abnormal
CC stimulation of endothelial cells; as a birth control agent; and in the
CC treatment of diseases that have angiogenesis as a pathological
CC consequence (see AAW94036 for details on the various diseases the
CC plasminogen fragments can be used to treat). The nucleotide sequences
CC encoding the plasminogen fragments can also be used for gene therapy. The
CC products can be used for the production of antibodies and in detection
CC and diagnosis. Sequences AAW94037 to W4041 represent angiotastatin
CC fragments (protein derivatives of angiotastatin or plasminogen, having an
CC endothelial cell proliferation activity) of murine, human, Rhesus,
CC porcine and bovine angiotastatin respectively. The kringle regions that
CC can be used in the invention are indicated in the features
XX
SQ Sequence 339 AA:
Query Match 99.7%; Score 1535; DB 2; Length 339;
Best Local Similarity 99.6%; Pred. No. 2.3e-90;
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 VYLSECKTGNKNGKRYGTMSTKNGITCOKWSTSPHRRPSPATHPSEGLEENYCRNPN 60
Db 1 VYLSECKTGNKNGKRYGTMSTKNGITCOKWSTSPHRRPSPATHPSEGLEENYCRNPN 60
QY 61 DPOGFWCYTTDPEKRYDYCDILECEECMHCSENYDGKISKTWGSLGECQAWDSOSPFAH 120

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DB 61 DPGSPWCYTTPDPERKYDYCDIIECEECHECHGSENGDGIKSKTMSGLECAMOSQSPHAA 120
QY 121 GYIPSKFPKNLKKYCNCRNPDRRLRPMWCFPTTDNKKMELCDIRCTTPPSSGPTVQCLK 180
DB 121 GYIPSKFPKNLKKYCNCRNPDRRLRPMWCFPTTDNKKMELCDIRCTTPPSSGPTVQCLK 180
QY 181 GTGENTRGNAVAVTSGHTCOHMSAQTPTHRTPEPNPCKNDENYCRNPDGKRAWCHT 240
DB 181 GTGENTRGNAVAVTSGHTCOHMSAQTPTHRTPEPNPCKNDENYCRNPDGKRAWCHT 240
QY 241 TNSQVRWEYCKIIPSCDSSPV 260
DB 241 TNSQVRWEYCKIIPSCDSSPV 260

RESULT 11
AAMS0518
ID AAMS0518 standard; protein; 339 AA.
AC AAMS0518;
XX
DT 12-MAR-2002 (first entry)
DE Human angiotactin.
XX
KM Angiotactin; plasminogen; human; angiogenesis; endothelial cell;
cell proliferation; inhibitor; tumour; antiproliferative; cytostatic;
vasoconstrictor; antitumour; dermatological; antiinflammatory; antidiabetic;
antithrombotic; antiatherosclerotic; ophthalmological; vulnery; anticancer;
antibacterial; antiatherosclerotic; gynaecological; antipruritic;
KM cardiant; contraceptive; therapy.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Region 6..255
FT /label= Kringle-1-3
FT /label= Kringle-1-2
FT /label= Kringle-1-1
FT /label= Kringle-2-3
FT /label= Kringle-2
FT /label= Kringle-2
FT /label= Kringle-3
XX
XX US2001029246-A1.
XX
XX 11-OCT-2001.
XX
XX 16-FEB-2001; 2001US-00788142.
XX
XX 30-MAY-1997; 97US-00866735.
XX 24-APR-1998; 98US-00866028.
XX 11-MAY-1999; 99US-00309821.
XX 22-JUN-1999; 99US-00338387.
XX
XX (OREI/) O'REILLY M S.
XX (FOLK/) FOLKMAN M J.
XX (CAOY/) CAO Y.
XX
XX O'reilly MS, Folkman MJ, Cao Y;
XX
XX MPI; 2001-647990/74.
XX
XX Inhibiting endothelial cell proliferation, useful for treating angiogenic
XX -mediated diseases such as cancer, arthritis, comprises administering
XX plasminogen fragment corresponding to kringle structures of plasminogen
XX molecule.
XX

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```

PS Example 27; Fig 2A-C; 70pp; English.
XX
CC The present sequence is that of human angiotactin. A claimed method of
CC inhibiting endothelial cell proliferation involves administering a
CC plasminogen fragment (PF) having an amino acid sequence similar to the
CC kringle 1-5 region of a plasminogen molecule. This includes a protein,
CC termed angiotactin, defined by its ability to overcome the angiogenic
CC activity of endogenous growth factors and by its amino acid sequence
CC homology and structural similarity to an internal portion of plasminogen,
CC beginning at approximately amino acid 98. The PF is preferably derived
CC from mouse, human, Rhesus monkey, pig or cattle (see AAMS0516-21). It is
CC used in methods and compositions for the treatment of an angiogenic-
CC mediated disease, including haemangioma, solid tumours, blood-borne
CC tumours, leukaemia, metastasis, telangiectasia, psoriasis,
CC atherosclerosis, scleroderma, pyogenic granuloma, myocardial
CC angiogenesis, Crohn's disease, plaque neovascularisation, coronary
CC collateral, cerebral collateral, arteriovenous malformations, ischaemic
CC limb angiogenesis, corneal diseases, rubeosis, neovascular glaucoma,
CC diabetic retinopathy, corneal graft rejection, retrolental fibroplasia,
CC haemophilic joints, rheumatoid arthritis, diabetic neovascularisation,
CC Osler-Webber syndrome, macular degeneration, wound healing, peptic ulcer,
CC Helicobacter pylori related diseases, fractures, keloids, vasculogenesis,
CC haematopoiesis, ovulation, menstruation, placental and cat scratch
CC fever. Angiotactin is also useful as a birth control agent by preventing
CC vasculature required for embryo implantation. The compositions are
CC particularly useful for treating or repressing the growth of tumours.
CC Administration of angiotactin to a human or animal with prevascularised
CC metastasised tumours will prevent the growth or expansion of those
CC tumours. Gene therapy methods are also included in the invention
XX
SQ Sequence 339 AA;

```

```

QY 1 VYISECTGNGKNGYKMGSTKNGITGQKWSSTSPHRRPSPATHPSEGLEENYCRNPDN 60
DB 1 VYISECTGNGKNGYKMGSTKNGITGQKWSSTSPHRRPSPATHPSEGLEENYCRNPDN 60
QY 61 DPGSPWCYTTPDPERKYDYCDIIECEECHECHGSENGDGIKSKTMSGLECAMOSQSPHAA 120
DB 61 DPGSPWCYTTPDPERKYDYCDIIECEECHECHGSENGDGIKSKTMSGLECAMOSQSPHAA 120
QY 121 GYIPSKFPKNLKKYCNCRNPDRRLRPMWCFPTTDNKKMELCDIRCTTPPSSGPTVQCLK 180
DB 121 GYIPSKFPKNLKKYCNCRNPDRRLRPMWCFPTTDNKKMELCDIRCTTPPSSGPTVQCLK 180
QY 181 GTGENTRGNAVAVTSGHTCOHMSAQTPTHRTPEPNPCKNDENYCRNPDGKRAWCHT 240
DB 181 GTGENTRGNAVAVTSGHTCOHMSAQTPTHRTPEPNPCKNDENYCRNPDGKRAWCHT 240
QY 241 TNSQVRWEYCKIIPSCDSSPV 260
DB 241 TNSQVRWEYCKIIPSCDSSPV 260

RESULT 12
ADG47024
ID ADG47024 standard; protein; 339 AA.
AC ADG47024;
XX
DT 11-MAR-2004 (first entry)
DE Human angiotactin protein.
XX
XX Angiotactin; cell proliferation; angiogenic-mediated disease; cancer;
XX arthritis; macular degeneration; diabetic retinopathy; psoriasis;
XX scleroderma; Crohn's disease; wounds; peptic ulcer; fracture;
XX gene therapy; plasminogen; cytostatic; ophthalmological; dermatological;
XX antiinflammatory; vulnery; human.
XX

```

OS	Homo sapiens.
XX	
PN	US2003064926-A1.
XX	
PD	03-APR-2003.
XX	
PF	22-APR-2002; 2002US-00127066.
XX	
PR	26-APR-1994; 94US-00248629.
PR	20-OCT-1994; 94US-00336786.
PR	26-APR-1995; 95US-00429743.
PR	08-MAR-1996; 96US-00612789.
PR	30-MAY-1997; 97US-00866735.
PR	24-APR-1998; 98US-00066026.
PR	11-MAY-1999; 99US-00309821.
PR	17-JUN-1999; 99US-00335325.
PR	22-JUN-1999; 99US-00383887.
PR	16-FEB-2001; 2001US-00788142.
XX	
PA	(FOLK/) FOLKMAN M J.
PT	(OREI/) O'REILLY M S.
PA	(CAOY/) CAO Y.
PA	(SIMK/) SIM K L.
XX	
PI	Folkman MJ, O'reilly MS, Cao Y, Sim KL;
XX	
DR	WPI: 2003-540796/51.
XX	
PT	Inhibiting endothelial cell proliferation, useful for treating cancer,
PT	arthritis or diabetic retinopathy, comprises administering to an
PT	endothelial cell a proliferation-inhibiting amount of an angiotatin
PT	fragment.
XX	
PS	Example 27; SEQ ID NO 3; 96pp; English.
XX	
CC	The present invention relates to endothelial inhibitors called
CC	angiotatin which reversibly inhibit proliferation of endothelial cells.
CC	The invention is useful for diagnosing and treating angiogenic-mediated
CC	diseases such as cancer, arthritis, macular degeneration, diabetic
CC	retinopathy, psoriasis, scleroderma, Crohn's disease, wounds, peptic
CC	ulcer and fractures. The invention is also useful in gene therapy. The
CC	present sequence is the human angiotatin protein.
XX	
XX	Sequence 339 AA;

Query Match	99.7%	Score 1535	DB 7	Length 339
Best Local Similarity	99.6%	Pred. No. 2.3e-90		
Matches 259	Conservative	0	Mismatches 1	Indels 0
			Gaps 0	
QY	1	YLSECKTKGNKKNYGTMSKTNGTTCQKMSSTSPHRPSPATPSBGLSEENYCRNPDN	60	
Db	1	YLSECKTKGNKKNYGTMSKTNGTTCQKMSSTSPHRPSPATPSBGLSEENYCRNPDN	60	
QY	61	DPQSPWCYTTDPEKRYDYCDLIECEECHMGSGENYDCKISKTMSGLECOAMDSSPHAH	120	
Db	61	DPQSPWCYTTDPEKRYDYCDLIECEECHMGSGENYDCKISKTMSGLECOAMDSSPHAH	120	
QY	121	GYISKSPFNKKULKKNYCNRNPPRELAPMCFTTDPNKRMLCDIPRCTTDPSSSGPTYYCLK	180	
Db	121	GYISKSPFNKKULKKNYCNRNPPRELAPMCFTTDPNKRMLCDIPRCTTDPSSSGPTYYCLK	180	
QY	181	GTGSENYGNVAVVTUSGHTCOHMSAOTPTHTERTPENPFCNKULDEYGCNPPGKAPWCHT	240	
Db	181	GTGSENYGNVAVVTUSGHTCOHMSAOTPTHTERTPENPFCNKULDEYGCNPPGKAPWCHT	240	
QY	241	TNSOVRMEYCKIPSCDSSPV 260		
Db	241	TNSOVRMEYCKIPSCDSSPV 260		

RESULT 13  
ADM11543  
ID ADM11543 standard; protein; 339 AA

XX	AC	ADM11543;
XX	AD	
XX	AE	
XX	AF	
XX	AG	
XX	AA	20-MAY-2004 (first entry)
DE	XX	Human plasminogen fragment (angiotatin).
XX	XX	
KW	KW	endothelial cell proliferation; plasminogen; kringle 1-5;
KW	KW	angiogenic-mediated disease; cancer; rheumatoid arthritis; psoriasis;
KW	KW	diabetic retinopathy; macular degeneration; corneal graft rejection;
KW	KW	neovascular glaucoma; retrolental fibroplasia; rubecosis;
KW	KW	Oster-Weber syndrome; myocardial angiogenesis; murine; human; Rhesus;
KW	KW	porcine; bovine; angiotatin.
XX	XX	
OS	OS	Homo sapiens.
XX	XX	
PN	PN	US2004023877-A1.
XX	XX	
PD	PD	05-FEB-2004.
XX	XX	
PF	PF	27-MAR-2003; 2003US-00401108.
XX	XX	
PR	PR	26-APR-1994; 94US-00248629.
PR	PR	20-OCT-1994; 94US-00326785.
PR	PR	26-APR-1995; 95US-00429743.
PR	PR	08-MAR-1996; 96US-00612788.
PR	PR	30-MAY-1997; 97US-00866735.
PR	PR	12-DEC-1997; 97US-00989477.
PR	PR	24-APR-1998; 98US-00066028.
PR	PR	11-MAY-1999; 99US-00309821.
PR	PR	22-JUN-1999; 99US-00338387.
PR	PR	16-FEB-2001; 2001US-00788142.
XX	XX	
PA	PA	(OREI/) O'REILLY M S.
PA	PA	(FOLK/) FOLKMAN M J.
PA	PA	(CAOV/) CAO Y.
XX	XX	
F1	F1	O'reilly MS, Folkman MJ, Cao Y;
XX	XX	
DR	DR	WPI; 2004-142673/14.
PT	PT	New composition comprising an isolated nucleotide sequence that codes for
PT	PT	a plasminogen fragment, useful for treating angiogenesis-dependent
PT	PT	diseases including cancer, rheumatoid arthritis, psoriasis or macular
PT	PT	degeneration.
XX	XX	
PS	PS	Example 18; SEQ ID NO 3; 78bp; English.
XX	XX	
CC	CC	The invention relates to a method of inhibiting endothelial cell
CC	CC	proliferation, comprising administering to an endothelial cell a
CC	CC	plasminogen fragment having an amino acid sequence similar to that of the
CC	CC	kringle 1-5 region of plasminogen. The plasminogen fragment is derived
CC	CC	from murine, human, Rhesus, porcine or bovine plasminogen. Also included
CC	CC	are the following: (1) a method of treating a mammal with an angiogenic-
CC	CC	mediated disease; (2) a therapeutic composition for inhibiting
CC	CC	endothelial cell proliferation comprising a pharmaceutical excipient and
CC	CC	the plasminogen fragment; and (3) a method of expressing a plasminogen
CC	CC	fragment having an endothelial cell proliferation inhibiting activity.
CC	CC	The method is useful for treating angiogenesis-dependent diseases
CC	CC	including cancer. Angiogenesis-mediated diseases also include rheumatoid
CC	CC	arthritis, psoriasis, diabetic retinopathy, macular degeneration, corneal
CC	CC	graft rejection, neovascular glaucoma, retrolental fibroplasia, rubecosis,
CC	CC	Oster-Weber syndrome or myocardial angiogenesis. The present sequence
CC	CC	represents human plasminogen fragment (angiotatin).
XX	XX	
Q0	Q0	Sequence 339 AA;

Query Match	99.7%	Score 1535	DB 8	Length 339
Best Local Similarity	99.6%	Pred. No. 2.3e-90		
Matches 259	Conservative	0	Mismatches 1	Indels 0
QY	1	VYLSECTGNGKRYRGCMSTKXGJGTCQKKSSSTSPHPRRSPATHPSEGLEENYCRPND	60	



Db 1 VYLSECKTGNGKNYRGTMSTKNGITCQKWSSTSPHPRPSPATHPSEGLEENYCRNPND 60  
 Qy 61 DPGPWCYTTDPKRYDYCDILECEBECMHCSENYDGKISKTMGLGECQAMDSQSPH 120  
 Db 61 DPGPWCYTTDPKRYDYCDILECEBECMHCSENYDGKISKTMGLGECQAMDSQSPH 120  
 Qy 121 GYIPSKFPNNKLNKKNYCRNPDRRLRPMCFCTTDPKRWELCDIPRCTPPSSGPTQCLK 180  
 Db 121 GYIPSKFPNNKLNKKNYCRNPDRRLRPMCFCTTDPKRWELCDIPRCTPPSSGPTQCLK 180  
 Qy 181 GTGENYRGNAVAVTSGHTCQWSAQTPHTHERTPENPCKNLDENYCRNPDGKRAPWCHT 240  
 Db 181 GTGENYRGNAVAVTSGHTCQWSAQTPHTHERTPENPCKNLDENYCRNPDGKRAPWCHT 240  
 Qy 241 TNSQVRWEYCKIPSCDSSPV 260  
 Db 241 TNSQVRWEYCKIPSCDSSPV 260  
 RESULT 14  
 ID AAY70255 standard; protein, 363 AA.  
 AC AAY70255;  
 XX 06-JUN-2000 (first entry)  
 DT  
 XX Human angiogenesis inhibitor, angiotatin.  
 DE Human, immunoglobulin gamma Fc fragment; angiotatin; immunofusin;  
 KW angiogenesis; inhibitor; cytoactive; antithrombotic; antiatheritic;  
 KW antiproliferative; antidiabetic; ophthalmological; immunosuppressant;  
 KW vasodilator; treatment; antiarteriosclerosis; tumour;  
 KW metastasis; atherosclerosis; psoriasis; rheumatoid arthritis;  
 KW ocular angiogenic disease; diabetic retinopathy; macular degeneration;  
 KW myocardial angiogenesis; plaque neovascularization; telangiectasia;  
 KW wound granulation; keloid scar; gene therapy.  
 KW  
 OS Homo sapiens.  
 XX  
 XX WO200011033-A2.  
 XX  
 XX 02-MAR-2000.  
 PD  
 XX 25-AUG-1999; 99WO-US019329.  
 PF  
 XX 25-AUG-1998; 98US-0097883P.  
 PR  
 XX (LEXI-) LEXINGEN PHARM CORP.  
 PA  
 XX Lo K, Li Y, Gillies SD;  
 PI  
 XX WPI: 2000-237616/20.  
 DR N-PSDB; AA251295.  
 XX  
 XX Novel fusion protein of angiotatin or endostatin and an immunoglobulin  
 PT FC region, useful for treating conditions mediated by angiogenesis, such  
 PT as rheumatoid arthritis, tumors and macular degeneration.  
 XX  
 XX Example 4; Page 45-46; 68pp; English.  
 PS  
 XX The patent discloses a DNA molecule encoding a fusion protein comprising  
 CC a signal sequence, an immunoglobulin Fc region, and an angiogenesis  
 CC inhibitor selected from angiotatin, endostatin, a plasminogen fragment  
 CC having angiotatin activity, a collagen XVIII fragment having endostatin  
 CC activity, or combinations of them. The fusion protein (immunofusin) is  
 CC used to inhibit angiogenesis and to treat diseases or conditions mediated  
 CC by angiogenesis. Conditions that may be treated include solid tumors,  
 CC blood born tumors, tumour metastasis, benign tumors including  
 CC haemangiomas, acoustic neuromas, neurofibromas, trachomas and pyrogenic  
 CC granulomas, rheumatoid arthritis, psoriasis, ocular angiogenic diseases  
 CC e.g. diabetic retinopathy, retinopathy of prematurity, macular  
 CC degeneration, corneal graft rejection, neovascular glaucoma, retrolental

CC fibroplasia, rubecosis and Osler-Webber syndrome; myocardial angiogenesis,  
 CC plaque neovascularization, telangiectasia, haemophilic joints,  
 CC angiodioma, wound granulation, and excessive or abnormal stimulation of  
 CC endothelial cells, intestinal cells, atherosclerosis, sclerodermal and  
 CC hypertrophic scars, i.e. keloid scars. The DNA constructs may be used in  
 CC gene therapy. The present sequence is a human angiotatin used in the  
 CC construction of immunofusin containing human immunoglobulin gamma (IgG)  
 CC Fc fragment  
 XX  
 SQ Sequence 363 AA;  
 Query Match 99.7%; Score 1535; DB 3; Length 363;  
 Best Local Similarity 99.6%; Pred. No. 2.5e-90;  
 Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Qy 1 VYLSECKTGNGKNYRGTMSTKNGITCQKWSSTSPHPRPSPATHPSEGLEENYCRNPND 60  
 Db 2 VYLSECKTGNGKNYRGTMSTKNGITCQKWSSTSPHPRPSPATHPSEGLEENYCRNPND 61  
 Qy 61 DPGPWCYTTDPKRYDYCDILECEBECMHCSENYDGKISKTMGLGECQAMDSQSPH 120  
 Db 62 DPGPWCYTTDPKRYDYCDILECEBECMHCSENYDGKISKTMGLGECQAMDSQSPH 121  
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 Qy 181 GTGENYRGNAVAVTSGHTCQWSAQTPHTHERTPENPCKNLDENYCRNPDGKRAPWCHT 240  
 Db 182 GTGENYRGNAVAVTSGHTCQWSAQTPHTHERTPENPCKNLDENYCRNPDGKRAPWCHT 241  
 Qy 241 TNSQVRWEYCKIPSCDSSPV 260  
 Db 242 TNSQVRWEYCKIPSCDSSPV 261  
 RESULT 15  
 ID AAY02106 standard; protein, 364 AA.  
 AC AAY02106;  
 XX 16-JUL-1999 (first entry)  
 DT  
 XX A multifunctional protein of the invention.  
 DE  
 XX Angiotatin; endostatin; interferon; thrombospondin;  
 KW interferon-inducible protein; platelet factor 4; anti-angiogenic;  
 KW anti-tumor; multifunctional protein; angiogenic-mediated disease; cancer;  
 KW diabetic retinopathy; macular degeneration; arthritis;  
 KW tumor cell production.  
 KW  
 OS Synthetic.  
 XX  
 XX Homo sapiens.  
 XX  
 XX WO9916889-A1.  
 PN  
 XX 08-APR-1999.  
 PD  
 XX 30-SEP-1998; 98WO-US020464.  
 PF  
 XX 01-OCT-1997; 97US-0060609P.  
 PR  
 XX (SEAR) SEARLE & CO G D.  
 PA  
 XX Bolanowski MA, Caparon MH, Casperson GF, Gregory SA, Klein BK;  
 PI McEarn JP;  
 PI WPI: 1999-255098/21.  
 DR  
 XX New multifunctional proteins useful for treating angiogenic-mediated  
 PT diseases.  
 PT  
 XX

PS Claim 5; Page 101-102; 121pp; English.

XX The specification describes multifunctional proteins which comprise  
CC combinations of angiotensin, endostatin, interferon, thrombospondin,  
CC interferon-inducible protein and platelet factor 4, and have anti-  
CC angiogenic and/or anti-tumor activity. The multifunctional protein may  
CC exhibit useful properties such as having similar or greater biological  
CC activity when compared to a single factor or by having improved half-life  
CC or decreased adverse side effects, or a combination of these properties.  
CC The proteins can be used for treating an angiogenic-mediated disease,  
CC e.g. cancer, diabetic retinopathy, macular degeneration, or arthritis.  
CC They can also be used for inhibiting the production of tumor cells  
CC (characteristic of lung, breast, ovarian, prostate, pancreatic, gastric,  
CC colon, renal, bladder cancers; melanoma, hepatoma, sarcoma and lymphoma)  
CC in a patient and for inhibiting tumor growth. The present sequence  
CC represents a multifunctional protein of the invention

XX Sequence 364 AA;

Query Match 99.7%; Score 1535; DB 2; Length 364;  
Best Local Similarity 99.6%; Pred. No. 2.5e-90;  
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VYLSECKTGNGKNTGKMTSKTNGITCQKMSSTSPHRRPSPATHPSGEGLENYCRNPDN 60  
Db 3 VYLSECKTGNGKNTGKMTSKTNGITCQKMSSTSPHRRPSPATHPSGEGLENYCRNPDN 62  
QY 61 DPGPMCTTDPKRYDYCDILECEBECMHSGENYDGI SKTMSGLECOAMDQSPPAH 120  
Db 63 DPGPMCTTDPKRYDYCDILECEBECMHSGENYDGI SKTMSGLECOAMDQSPPAH 122  
QY 121 GYIPSKFPNNKLLKKNYCRNPDLRPMCFITDPNKRWELCDIPRCTPPPSGPTYOCLK 180  
Db 123 GYIPSKFPNNKLLKKNYCRNPDLRPMCFITDPNKRWELCDIPRCTPPPSGPTYOCLK 182  
QY 181 GTGENYKGNVAVTSGHTCQKMSAQTPTHTERTPEPNPCXLDENYCRNPDGKRAPWCHT 240  
Db 183 GTGENYKGNVAVTSGHTCQKMSAQTPTHTERTPEPNPCXLDENYCRNPDGKRAPWCHT 242  
QY 241 TNSQVMEYCKIPSCDSSPV 260  
Db 243 TNSQVMEYCKIPSCDSSPV 262

Search completed: July 27, 2005; 03:29:02  
Job time : 75 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 27, 2005, 03:30:16; Search time 157 Seconds

(without alignments)  
644.191 Million cell updates/sec

Title: US-09-502-176-2

Perfect score: 1540

Sequence: 1 VIISECKTNGKNGKRYGTMSK.....TNSQVWEYCKIIPSCDSSEV 260

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 1741741 seqs, 388992284 residues

Total number of hits satisfying chosen parameters: 1741741

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: Published Applications, AA:

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2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*  
3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep.\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1540	100.0	260	14 US-10-131-241-61	Sequence 61, Appl
2	1535	99.7	303	16 US-10-810-262-11	Sequence 11, Appl
3	1535	99.7	339	9 US-09-788-142-3	Sequence 3, Appl
4	1535	99.7	339	9 US-09-761-120-3	Sequence 3, Appl
5	1535	99.7	339	9 US-09-335-325-3	Sequence 3, Appl
6	1535	99.7	339	14 US-10-131-241-3	Sequence 3, Appl
7	1535	99.7	339	14 US-10-127-066-3	Sequence 3, Appl
8	1535	99.7	339	15 US-10-402-364-3	Sequence 3, Appl
9	1535	99.7	339	15 US-10-401-108-3	Sequence 3, Appl
10	1535	99.7	363	14 US-10-292-418-11	Sequence 11, Appl
11	1535	99.7	378	9 US-09-873-676-1	Sequence 1, Appl

12	1535	99.7	378	9 US-09-335-325-42	Sequence 42, Appl
13	1535	99.7	378	14 US-10-131-241-42	Sequence 42, Appl
14	1535	99.7	378	14 US-10-127-066-42	Sequence 42, Appl
15	1535	99.7	391	14 US-10-304-287-7	Sequence 7, Appl
16	1535	99.7	391	15 US-10-415-012-1	Sequence 1, Appl
17	1535	99.7	391	16 US-10-735-577-7	Sequence 7, Appl
18	1535	99.7	394	14 US-10-304-287-8	Sequence 8, Appl
19	1535	99.7	394	15 US-10-415-012-2	Sequence 2, Appl
20	1535	99.7	394	16 US-10-735-577-8	Sequence 8, Appl
21	1535	99.7	484	15 US-10-135-872B-7	Sequence 7, Appl
22	1535	99.7	567	16 US-10-741-601-413	Sequence 413, App
23	1535	99.7	569	9 US-09-946-893-5	Sequence 5, Appl
24	1535	99.7	571	9 US-09-946-893-8	Sequence 8, Appl
25	1535	99.7	576	9 US-09-946-893-6	Sequence 6, Appl
26	1535	99.7	579	16 US-10-449-609-7	Sequence 7, Appl
27	1535	99.7	714	15 US-10-415-012-8	Sequence 8, Appl
28	1535	99.7	714	18 US-10-503-910-18	Sequence 18, Appl
29	1535	99.7	791	9 US-09-967-386-1	Sequence 1, Appl
30	1535	99.7	791	14 US-10-304-287-1	Sequence 1, Appl
31	1535	99.7	791	15 US-10-360-101-257	Sequence 257, App
32	1535	99.7	791	16 US-10-778-423-1	Sequence 1, Appl
33	1535	99.7	791	16 US-10-753-646-1	Sequence 1, Appl
34	1535	99.7	791	16 US-10-735-577-1	Sequence 1, Appl
35	1535	99.7	791	17 US-10-729-475-10	Sequence 10, Appl
36	1535	99.7	799	18 US-10-503-910-17	Sequence 17, Appl
37	1535	99.7	803	18 US-10-503-910-10	Sequence 10, Appl
38	1535	99.7	810	9 US-09-946-893-2	Sequence 2, Appl
39	1535	99.7	810	14 US-10-193-656-2	Sequence 2, Appl
40	1535	99.7	810	14 US-10-237-144-1	Sequence 1, Appl
41	1535	99.7	810	15 US-10-135-872B-4	Sequence 4, Appl
42	1535	99.7	810	15 US-10-450-976-2	Sequence 2, Appl
43	1535	99.7	810	15 US-10-415-012-2	Sequence 4, Appl
44	1535	99.7	810	15 US-10-741-601-409	Sequence 409, App
45	1535	99.7	810	16 US-10-741-601-409	Sequence 409, App

## ALIGNMENTS

RESULT 1  
US-10-131-241-61  
Sequence 61, Application US/10131241  
Publication No. US20030012725A1  
GENERAL INFORMATION: John W.  
APPLICANT: Holladay, John W.  
TITLE OF INVENTION: Compositions and Methods for Inhibiting Endothelial Cell Proliferation  
TITLE OF INVENTION: and Regulating Angiogenesis Using Cancer Markers  
FILE REFERENCE: 05213-0344 43170-271565  
CURRENT APPLICATION NUMBER: US/10/131,241  
PRIOR FILING DATE: 2002-07-22  
PRIOR APPLICATION NUMBER: US 09/413,049  
PRIOR FILING DATE: 1999-10-06  
PRIOR APPLICATION NUMBER: US 09/316,802  
PRIOR FILING DATE: 1999-05-21  
PRIOR APPLICATION NUMBER: US 60/086,586  
PRIOR FILING DATE: 1998-05-22  
NUMBER OF SEQ ID NOS: 65  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 61  
LENGTH: 260  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-131-241-61

Query Match 100.0%; Score 1540; DB 14; Length 260;  
Best Local Similarity 100.0%; Pred. No. 2e-120;  
Matches 260; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 VIISECKTNGKNGKRYGTMSKNGITCKQWSSTSPRPSPATPSPSEGLNNYCRNP 60  
DB 1 VIISECKTNGKNGKRYGTMSKNGITCKQWSSTSPRPSPATPSPSEGLNNYCRNP 60

Qy 61 DPGWCYTTDPKRYDYCDILCEBEECHMGSGENYDGKISKTMSGLECAMDSQSPH 120  
Db 61 DPGWCYTTDPKRYDYCDILCEBEECHMGSGENYDGKISKTMSGLECAMDSQSPH 120  
Qy 121 GYISKFPKNKLLKKNYCNPNRPRELRPMWCTTDPNKRWELCDIPRCTPPSSGPTYQCL 180  
Db 121 GYISKFPKNKLLKKNYCNPNRPRELRPMWCTTDPNKRWELCDIPRCTPPSSGPTYQCL 180  
Qy 181 GTGENYGNVAVTYSGHTCOHWSAOTPHHTERTPENPCKNLDENYCRNPDGKAPWCHT 240  
Db 181 GTGENYGNVAVTYSGHTCOHWSAOTPHHTERTPENPCKNLDENYCRNPDGKAPWCHT 240  
Qy 241 TNSQVMEYCKIPSCDSSPV 260  
Db 241 TNSQVMEYCKIPSCDSSPV 260

RESULT 2  
US-10-810-262-11  
Sequence 11, Application US/10810262  
Publication No. US20040234505A1  
GENERAL INFORMATION:  
APPLICANT: NAVILOR, STUART  
APPLICANT: KINGSMAN, SUSAN MARY  
APPLICANT: BINLEY, KATIE  
TITLE OF INVENTION: POLYNUCLEOTIDE CONSTRUCTS AND USES THEREOF  
FILE REFERENCE: 674523-2029-1  
CURRENT APPLICATION NUMBER: US/10/810, 262  
CURRENT FILING DATE: 2004-03-26  
PRIOR APPLICATION NUMBER: 09/787,562  
PRIOR FILING DATE: 2001-07-06  
PRIOR APPLICATION NUMBER: PCT/GB99/03181  
PRIOR FILING DATE: 1999-09-22  
PRIOR APPLICATION NUMBER: PCT/GB98/02885  
PRIOR FILING DATE: 1998-09-23  
PRIOR APPLICATION NUMBER: GB 9901906.9  
PRIOR FILING DATE: 1999-01-28  
PRIOR APPLICATION NUMBER: GB 9903538.8  
PRIOR FILING DATE: 1999-02-16  
NUMBER OF SEQ ID NOS: 34  
SOFTWARE: PatentIn Ver. 3.2  
SEQ ID NO 11  
LENGTH: 303  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-810-262-11

Query Match 99.7%; Score 1535; DB 16; Length 303;  
Best Local Similarity 99.6%; Pred. No. 6.1e-120;  
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VYLSECKTGNGKNGYGTGKNGITCQKWSSTSPHPRFSPATHPSBGLSENYCRNPDN 60  
Db 33 VYLSECKTGNGKNGYGTGKNGITCQKWSSTSPHPRFSPATHPSBGLSENYCRNPDN 92  
Qy 61 DPGWCYTTDPKRYDYCDILCEBEECHMGSGENYDGKISKTMSGLECAMDSQSPH 120  
Db 93 DPGWCYTTDPKRYDYCDILCEBEECHMGSGENYDGKISKTMSGLECAMDSQSPH 152  
Qy 121 GYISKFPKNKLLKKNYCNPNRPRELRPMWCTTDPNKRWELCDIPRCTPPSSGPTYQCL 180  
Db 153 GYISKFPKNKLLKKNYCNPNRPRELRPMWCTTDPNKRWELCDIPRCTPPSSGPTYQCL 212  
Qy 181 GTGENYGNVAVTYSGHTCOHWSAOTPHHTERTPENPCKNLDENYCRNPDGKAPWCHT 240  
Db 213 GTGENYGNVAVTYSGHTCOHWSAOTPHHTERTPENPCKNLDENYCRNPDGKAPWCHT 272  
Qy 241 TNSQVMEYCKIPSCDSSPV 260  
Db 273 TNSQVMEYCKIPSCDSSPV 292

RESULT 3

US-09-788-142-3  
Sequence 3, Application US/09788142  
Patent No. US20010029246A1  
GENERAL INFORMATION:  
APPLICANT: Folkmann, M. Judah  
O'Reilly, Michael  
TITLE OF INVENTION: Angiostatin Fragments and Method of Use  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Jones & Askew, LLP  
STREET: 191 Peachtree Street, 37th Floor  
CITY: Atlanta  
STATE: Georgia  
COUNTRY: USA  
ZIP: 30303-1769  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US 09/788,142  
FILING DATE: 16-Feb-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/866,735  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Warren, William L.  
REGISTRATION NUMBER: 36,714  
REFERENCE/DOCKET NUMBER: 05940-0129  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (404) 818-3700  
TELEFAX: (404) 818-3799  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 339 amino acids  
TYPE: amino acid  
STRANDEDNESS: <Unknown>  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: N-terminal  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
IMMEDIATE SOURCE:  
CLONE: Angiostatin fragment  
SEQUENCE DESCRIPTION: SEQ ID NO: 3:  
US-09-788-142-3  
Query Match 99.7%; Score 1535; DB 9; Length 339;  
Best Local Similarity 99.6%; Pred. No. 6.9e-120;  
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VYLSECKTGNGKNGYGTGKNGITCQKWSSTSPHPRFSPATHPSBGLSENYCRNPDN 60  
Db 1 VYLSECKTGNGKNGYGTGKNGITCQKWSSTSPHPRFSPATHPSBGLSENYCRNPDN 60  
Qy 61 DPGWCYTTDPKRYDYCDILCEBEECHMGSGENYDGKISKTMSGLECAMDSQSPH 120  
Db 61 DPGWCYTTDPKRYDYCDILCEBEECHMGSGENYDGKISKTMSGLECAMDSQSPH 120  
Qy 121 GYISKFPKNKLLKKNYCNPNRPRELRPMWCTTDPNKRWELCDIPRCTPPSSGPTYQCL 180  
Db 121 GYISKFPKNKLLKKNYCNPNRPRELRPMWCTTDPNKRWELCDIPRCTPPSSGPTYQCL 180  
Qy 181 GTGENYGNVAVTYSGHTCOHWSAOTPHHTERTPENPCKNLDENYCRNPDGKAPWCHT 240  
Db 181 GTGENYGNVAVTYSGHTCOHWSAOTPHHTERTPENPCKNLDENYCRNPDGKAPWCHT 240  
Qy 241 TNSQVMEYCKIPSCDSSPV 260  
Db 241 TNSQVMEYCKIPSCDSSPV 260

Db 241 TNSOVRWEYCKIPSCDSSPV 260

RESULT 4

US-09-761-120-3  
Sequence 3, Application US/09761120  
Patent No. US20020037847A1

GENERAL INFORMATION:

APPLICANT: O'Reilly, M. Judah  
APPLICANT: Folkmann, Michael  
TITLE OF INVENTION: Nucleic Acids Encoding Kriingle 1-5 Region Fragments of Plasminogen  
FILE REFERENCE: 05940-0151 (43171-252068)  
CURRENT APPLICATION NUMBER: US/09/761,120  
CURRENT FILING DATE: 2001-01-16  
PRIOR APPLICATION NUMBER: 09/309,821  
PRIOR FILING DATE: 1999-05-11  
PRIOR APPLICATION NUMBER: 08/866,735  
PRIOR FILING DATE: 1997-05-30  
NUMBER OF SEQ ID NOS: 47  
SOFTWARE: Patentin version 3.0  
SEQ ID NO: 339  
LENGTH: 339  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-761-120-3

Query Match 99.7%; Score 1535; DB 9; Length 339;  
Best Local Similarity 99.6%; Pred. No. 6,9e-120;  
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VYLSECKTGNGKNGYRGTMSTKNGITCOKMSTSPHPRPSPATHPSSEGLEENYCRNPDN 60  
Db 1 VYLSECKTGNGKNGYRGTMSTKNGITCOKMSTSPHPRPSPATHPSSEGLEENYCRNPDN 60  
QY 61 DPQGWCTTDPPEKRYDYCDILECEBECMHGSGENYDGIKSTMSGLECOAMDOSPHAH 120  
Db 61 DPQGWCTTDPPEKRYDYCDILECEBECMHGSGENYDGIKSTMSGLECOAMDOSPHAH 120  
QY 121 GIYPSKFPNKNLKNYCRNPDRELPRWCFTTDPNKRWELCDIPRCTTTPSSGFTYQCLK 180  
Db 121 GIYPSKFPNKNLKNYCRNPDRELPRWCFTTDPNKRWELCDIPRCTTTPSSGFTYQCLK 180  
QY 181 GTGENYRGNAVAVTSGHTCOHMSAQTPTHTERTPEPFCXNLDENYCRNPDGKRAPWCHT 240  
Db 181 GTGENYRGNAVAVTSGHTCOHMSAQTPTHTERTPEPFCXNLDENYCRNPDGKRAPWCHT 240  
QY 241 TNSOVRWEYCKIPSCDSSPV 260  
Db 241 TNSOVRWEYCKIPSCDSSPV 260

RESULT 5

US-09-335-325-3  
Sequence 3, Application US/09335325  
Patent No. US20020164717A1

GENERAL INFORMATION:

APPLICANT: Folkmann, M. Judah  
APPLICANT: O'Reilly, Michael  
APPLICANT: Cao, Yihai  
APPLICANT: Sim, B. Kim Lee  
TITLE OF INVENTION: Angiostatin Fragments and Method of Use  
NUMBER OF SEQUENCES: 45  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Jones & Askew  
STREET: 191 Peachtree Street, 37th Floor  
CITY: Atlanta  
STATE: Georgia  
COUNTRY: U.S.  
ZIP: 30303-1769  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/335,325  
FILING DATE: 17-Jun-1999  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/612,788  
FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Warren, William L.  
REGISTRATION NUMBER: 36,714  
REFERENCE/DOCKET NUMBER: 05213-0126  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 404-818-3700  
TELEFAX: 404-818-3799

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:  
LENGTH: 339 amino acids  
TYPE: amino acid  
STRANDEDNESS: <Unknown>  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: N-terminal  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
IMMEDIATE SOURCE:  
CLONE: Angiostatin fragment  
SEQUENCE DESCRIPTION: SEQ ID NO: 3:  
US-09-335-325-3

Query Match 99.7%; Score 1535; DB 9; Length 339;  
Best Local Similarity 99.6%; Pred. No. 6,9e-120;  
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VYLSECKTGNGKNGYRGTMSTKNGITCOKMSTSPHPRPSPATHPSSEGLEENYCRNPDN 60  
Db 1 VYLSECKTGNGKNGYRGTMSTKNGITCOKMSTSPHPRPSPATHPSSEGLEENYCRNPDN 60  
QY 61 DPQGWCTTDPPEKRYDYCDILECEBECMHGSGENYDGIKSTMSGLECOAMDOSPHAH 120  
Db 61 DPQGWCTTDPPEKRYDYCDILECEBECMHGSGENYDGIKSTMSGLECOAMDOSPHAH 120  
QY 121 GIYPSKFPNKNLKNYCRNPDRELPRWCFTTDPNKRWELCDIPRCTTTPSSGFTYQCLK 180  
Db 121 GIYPSKFPNKNLKNYCRNPDRELPRWCFTTDPNKRWELCDIPRCTTTPSSGFTYQCLK 180  
QY 181 GTGENYRGNAVAVTSGHTCOHMSAQTPTHTERTPEPFCXNLDENYCRNPDGKRAPWCHT 240  
Db 181 GTGENYRGNAVAVTSGHTCOHMSAQTPTHTERTPEPFCXNLDENYCRNPDGKRAPWCHT 240  
QY 241 TNSOVRWEYCKIPSCDSSPV 260  
Db 241 TNSOVRWEYCKIPSCDSSPV 260

RESULT 6

US-10-131-241-3  
Sequence 3, Application US/10131241  
Publication No. US20030012792A1

GENERAL INFORMATION:

APPLICANT: Holaday, John W.  
APPLICANT: Fortlier, Anne H.  
TITLE OF INVENTION: Compositions and Methods for Inhibiting Endothelial Cell Proliferation  
TITLE OF INVENTION: and Regulating Angiogenesis Using Cancer Markers  
FILE REFERENCE: 05213-0344 43170-271565  
CURRENT APPLICATION NUMBER: US/10/131,241  
CURRENT FILING DATE: 2002-07-22  
PRIOR APPLICATION NUMBER: US 09/413,049  
PRIOR FILING DATE: 1999-10-06  
PRIOR APPLICATION NUMBER: US 09/316,802  
PRIOR FILING DATE: 1999-05-21

PRIOR APPLICATION NUMBER: US 60/086,586  
PRIOR FILING DATE: 1998-05-22  
NUMBER OF SEQ ID NOS: 65  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 3  
LENGTH: 339  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-131-241-3

Query Match 99.7%; Score 1535; DB 14; Length 339;  
Best Local Similarity 99.6%; Pred. No. 6,9e-120;  
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VYLSECKTGNGKRYGKMTGKNGITCOKWSSTSPHRRPSPATHPSEGLEENYCRPN 60  
DB 1 VYLSECKTGNGKRYGKMTGKNGITCOKWSSTSPHRRPSPATHPSEGLEENYCRPN 60  
QY 61 DPOGWCYTTDPKRYDYCDILECEECMHGSGENYDGIKSTMSGLECOAMDSOPHAH 120  
DB 61 DPOGWCYTTDPKRYDYCDILECEECMHGSGENYDGIKSTMSGLECOAMDSOPHAH 120  
QY 121 GIYPSKFPKNLKKYCRNPDELRLPWCCTTDPNKMELCDIPRCTPPSSGPTYQCLK 180  
DB 121 GIYPSKFPKNLKKYCRNPDELRLPWCCTTDPNKMELCDIPRCTPPSSGPTYQCLK 180  
QY 181 GTGENYRGNAVTVSGHTCOHWSAOTPHHTERTPENPCKNLDENYCRNPDGRAPWCHT 240  
DB 181 GTGENYRGNAVTVSGHTCOHWSAOTPHHTERTPENPCKNLDENYCRNPDGRAPWCHT 240  
QY 241 TNSQVRWEYCKIPSCDSSPV 260  
DB 241 TNSQVRWEYCKIPSCDSSPV 260

RESULT 7  
US-10-127-066-3  
Sequence 3, Application US/10127066  
Publication No. US20030064926A1  
GENERAL INFORMATION:  
APPLICANT: O'Reilly, Michael S.  
APPLICANT: Folkman, M. Judah  
APPLICANT: Cao, Kim Lee  
TITLE OF INVENTION: Angiostatin Fragments and Method of Use  
FILE REFERENCE: 05213-0612 43170-272529  
CURRENT APPLICATION NUMBER: US/10/127,066  
CURRENT FILING DATE: 2002-07-23  
NUMBER OF SEQ ID NOS: 45  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 3  
LENGTH: 339  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-127-066-3

Query Match 99.7%; Score 1535; DB 14; Length 339;  
Best Local Similarity 99.6%; Pred. No. 6,9e-120;  
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VYLSECKTGNGKRYGKMTGKNGITCOKWSSTSPHRRPSPATHPSEGLEENYCRPN 60  
DB 1 VYLSECKTGNGKRYGKMTGKNGITCOKWSSTSPHRRPSPATHPSEGLEENYCRPN 60  
QY 61 DPOGWCYTTDPKRYDYCDILECEECMHGSGENYDGIKSTMSGLECOAMDSOPHAH 120  
DB 61 DPOGWCYTTDPKRYDYCDILECEECMHGSGENYDGIKSTMSGLECOAMDSOPHAH 120  
QY 121 GIYPSKFPKNLKKYCRNPDELRLPWCCTTDPNKMELCDIPRCTPPSSGPTYQCLK 180  
DB 121 GIYPSKFPKNLKKYCRNPDELRLPWCCTTDPNKMELCDIPRCTPPSSGPTYQCLK 180  
QY 181 GTGENYRGNAVTVSGHTCOHWSAOTPHHTERTPENPCKNLDENYCRNPDGRAPWCHT 240

DB 181 GTGENYRGNAVTVSGHTCOHWSAOTPHHTERTPENPCKNLDENYCRNPDGRAPWCHT 240  
QY 241 TNSQVRWEYCKIPSCDSSPV 260  
DB 241 TNSQVRWEYCKIPSCDSSPV 260

RESULT 8  
US-10-402-364-3  
Sequence 3, Application US/10402364  
Publication No. US20040002459A1  
GENERAL INFORMATION:  
APPLICANT: O'Reilly, Michael  
APPLICANT: Folkman, M. Judah  
TITLE OF INVENTION: Nucleic Acids Encoding Kringling 1-5 Region Fragments of Plasminogen  
FILE REFERENCE: 05213-2151 (43170-252068)  
CURRENT APPLICATION NUMBER: US/10/402,364  
CURRENT FILING DATE: 2003-03-28  
PRIOR APPLICATION NUMBER: US/09/761,120A  
PRIOR FILING DATE: 2001-01-16  
PRIOR APPLICATION NUMBER: 09/309,821  
PRIOR FILING DATE: 1999-05-11  
PRIOR APPLICATION NUMBER: 08/866,735  
PRIOR FILING DATE: 1997-05-30  
NUMBER OF SEQ ID NOS: 52  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 3  
LENGTH: 339  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-402-364-3

Query Match 99.7%; Score 1535; DB 15; Length 339;  
Best Local Similarity 99.6%; Pred. No. 6,9e-120;  
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VYLSECKTGNGKRYGKMTGKNGITCOKWSSTSPHRRPSPATHPSEGLEENYCRPN 60  
DB 1 VYLSECKTGNGKRYGKMTGKNGITCOKWSSTSPHRRPSPATHPSEGLEENYCRPN 60  
QY 61 DPOGWCYTTDPKRYDYCDILECEECMHGSGENYDGIKSTMSGLECOAMDSOPHAH 120  
DB 61 DPOGWCYTTDPKRYDYCDILECEECMHGSGENYDGIKSTMSGLECOAMDSOPHAH 120  
QY 121 GIYPSKFPKNLKKYCRNPDELRLPWCCTTDPNKMELCDIPRCTPPSSGPTYQCLK 180  
DB 121 GIYPSKFPKNLKKYCRNPDELRLPWCCTTDPNKMELCDIPRCTPPSSGPTYQCLK 180  
QY 181 GTGENYRGNAVTVSGHTCOHWSAOTPHHTERTPENPCKNLDENYCRNPDGRAPWCHT 240  
DB 181 GTGENYRGNAVTVSGHTCOHWSAOTPHHTERTPENPCKNLDENYCRNPDGRAPWCHT 240  
QY 241 TNSQVRWEYCKIPSCDSSPV 260  
DB 241 TNSQVRWEYCKIPSCDSSPV 260

RESULT 9  
US-10-401-108-3  
Sequence 3, Application US/10401108  
Publication No. US20040023877A1  
GENERAL INFORMATION:  
APPLICANT: Folkman, M. Judah  
APPLICANT: O'Reilly, Michael  
TITLE OF INVENTION: Angiostatin Fragments and Method of Use  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSES: Jones & Askew, LLP  
STREET: 191 Peachtree Street, 37th Floor  
CITY: Atlanta  
STATE: Georgia  
COUNTRY: USA

```

; ZIP: 30303-1769
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/401,108
; FILING DATE: 27-Mar-2003
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/866,735
; FILING DATE: 30-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren, William L.
; REGISTRATION NUMBER: 36,714
; TELEPHONE: (404) 818-3700
; TELEFAX: (404) 818-3799
; TELECOMMUNICATION INFORMATION:
; REFERENCE/DOCKET NUMBER: 05940-0129
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 339 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; IMMEDIATE SOURCE:
; CLONE: Angiostatin fragment
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-401-108-3

Query Match          99.7%; Score 1535; DB 15; Length 339;
Best Local Similarity 99.6%; Pred. No. 6,9e-120;
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 VYLSECKTGNGKNYRGMTSKTNGITCOKWSSTSPHRRPSPATHPSEGLEENYCRNPND 60
Db 1 VILSECKTGNGKNYRGMTSKTNGITCOKWSSTSPHRRPSPATHPSEGLEENYCRNPND 60
QY 61 DPGPWCYTTDPEKRYDYCDILECEBECMHGSGENYDGKISKTMGSLGCQAMDSOPH 120
Db 61 DPGPWCYTTDPEKRYDYCDILECEBECMHGSGENYDGKISKTMGSLGCQAMDSOPH 120
QY 121 GYIPSKFPNKNLKNYCRNPDELRLPWCFTTDPNKRWELCDIPRCTPPSSGPTYQCL 180
Db 121 GYIPSKFPNKNLKNYCRNPDELRLPWCFTTDPNKRWELCDIPRCTPPSSGPTYQCL 180
QY 122 GYIPSKFPNKNLKNYCRNPDELRLPWCFTTDPNKRWELCDIPRCTPPSSGPTYQCL 180
Db 122 GYIPSKFPNKNLKNYCRNPDELRLPWCFTTDPNKRWELCDIPRCTPPSSGPTYQCL 180
QY 181 GTGENYRGNAVAVTSGHTCOHWSAQTPTHTERTPENPCKNIDENYCRNPDGRAPWCHT 240
Db 181 GTGENYRGNAVAVTSGHTCOHWSAQTPTHTERTPENPCKNIDENYCRNPDGRAPWCHT 240
QY 241 TNSQVMEYCKIIPSCDSSPV 260
Db 241 TNSQVMEYCKIIPSCDSSPV 260
;
; RESULT 10
; US-10-292-418-11
; Sequence 11, Application US/10292418
; Publication No. US20030139365A1
; GENERAL INFORMATION:
; APPLICANT: Lo, Kin-Ming
; APPLICANT: Li, Yue
; APPLICANT: Gillies, Stephen D
; TITLE OF INVENTION: Expression and Export of Angiogenesis Inhibitors as
; TITLE OF INVENTION: Immunofusins
; FILE REFERENCE: LEX-006C1

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; CURRENT APPLICATION NUMBER: US/10/292,418
; CURRENT FILING DATE: 2002-11-12
; PRIOR APPLICATION NUMBER: 09/383,315
; PRIOR FILING DATE: 1999-08-25
; PRIOR APPLICATION NUMBER: US 60/097,883
; PRIOR FILING DATE: 1998-08-25
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 11
; LENGTH: 363
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-292-418-11

Query Match          99.7%; Score 1535; DB 14; Length 363;
Best Local Similarity 99.6%; Pred. No. 7.5e-120;
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 VYLSECKTGNGKNYRGMTSKTNGITCOKWSSTSPHRRPSPATHPSEGLEENYCRNPND 60
Db 2 VYLSECKTGNGKNYRGMTSKTNGITCOKWSSTSPHRRPSPATHPSEGLEENYCRNPND 61
QY 61 DPGPWCYTTDPEKRYDYCDILECEBECMHGSGENYDGKISKTMGSLGCQAMDSOPH 120
Db 62 DPGPWCYTTDPEKRYDYCDILECEBECMHGSGENYDGKISKTMGSLGCQAMDSOPH 121
QY 121 GYIPSKFPNKNLKNYCRNPDELRLPWCFTTDPNKRWELCDIPRCTPPSSGPTYQCL 180
Db 122 GYIPSKFPNKNLKNYCRNPDELRLPWCFTTDPNKRWELCDIPRCTPPSSGPTYQCL 181
QY 181 GTGENYRGNAVAVTSGHTCOHWSAQTPTHTERTPENPCKNIDENYCRNPDGRAPWCHT 240
Db 182 GTGENYRGNAVAVTSGHTCOHWSAQTPTHTERTPENPCKNIDENYCRNPDGRAPWCHT 241
QY 241 TNSQVMEYCKIIPSCDSSPV 260
Db 242 TNSQVMEYCKIIPSCDSSPV 261
;
; RESULT 11
; US-09-873-676-1
; Sequence 1, Application US/09873676
; Patent No. US20020077289A1
; GENERAL INFORMATION:
; APPLICANT: Macdonald, Nicholas J.
; APPLICANT: Sim, Kim L.
; TITLE OF INVENTION: Angiostatin and Endostatin Binding Proteins and Methods of Use
; FILE REFERENCE: 05213-0378 (43170-259333)
; CURRENT FILING DATE: US/09/873,676
; PRIOR APPLICATION NUMBER: 2001-06-04
; PRIOR FILING DATE: 2000-06-02
; PRIOR APPLICATION NUMBER: US 60/209,065
; PRIOR FILING DATE: 2001-05-08
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 1
; LENGTH: 378
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-873-676-1

Query Match          99.7%; Score 1535; DB 9; Length 378;
Best Local Similarity 99.6%; Pred. No. 7.8e-120;
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 VYLSECKTGNGKNYRGMTSKTNGITCOKWSSTSPHRRPSPATHPSEGLEENYCRNPND 60
Db 6 VYLSECKTGNGKNYRGMTSKTNGITCOKWSSTSPHRRPSPATHPSEGLEENYCRNPND 65
QY 61 DPGPWCYTTDPEKRYDYCDILECEBECMHGSGENYDGKISKTMGSLGCQAMDSOPH 120
Db 66 DPGPWCYTTDPEKRYDYCDILECEBECMHGSGENYDGKISKTMGSLGCQAMDSOPH 125

```

QY 121 GYIPSKFPKXNKKYCRNPDLRPMWCTTDPNKRMECDIPRCTPPSSGPTYOCLK 180  
DB 126 GYIPSKFPKXNKKYCRNPDLRPMWCTTDPNKRMECDIPRCTPPSSGPTYOCLK 185  
QY 181 GTGENYRGNAVAVTSGHTCOHWSAOTPHHTERTPENPCKNIDENYCRNPDGKRAFWCHT 240  
DB 186 GTGENYRGNAVAVTSGHTCOHWSAOTPHHTERTPENPCKNIDENYCRNPDGKRAFWCHT 245  
QY 241 TNSQVMEYCKIPSCDSSPV 260  
DB 246 TNSQVMEYCKIPSCDSSPV 265

RESULT 12  
US-09-335-325-42  
Sequence 42, Application US/09335325  
Patent No. US20020164717A1  
GENERAL INFORMATION:  
APPLICANT: Folkman, M. Judah  
Gao, Yihai  
O'Reilly, Michael  
Siu, B. Kim Lee  
TITLE OF INVENTION: Angiostatin Fragments and Method of Use  
NUMBER OF SEQUENCES: 45  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Jones & Askew  
STREET: 191 Peachtree Street, 37th Floor  
CITY: Atlanta  
STATE: Georgia  
COUNTRY: U.S.  
ZIP: 30303-1769  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/335,325  
FILING DATE: 17-Jun-1999  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/612,788  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Warren, William L.  
REGISTRATION NUMBER: 36,714  
REFERENCE/DOCKET NUMBER: 05213-0126  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 404-818-3700  
TELEFAX: 404-818-3799  
INFORMATION FOR SEQ ID NO: 42:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 378 amino acids  
TYPE: amino acid  
STRANDEDNESS: <Unknown>  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: N-terminal  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
IMMEDIATE SOURCE:  
CLONE: K1-4BKLS  
SEQUENCE DESCRIPTION: SEQ ID NO: 42:  
US-09-335-325-42

Query Match 99.7%; Score 1535; DB 9; Length 378;  
Best Local Similarity 99.6%; Pred. No. 7.8e-120;  
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
1 VYLSECKTNGKXNYRGTMSTKNGITCOKWSSTSPHPRPSPATHPSEGLSENYCRNPDN 60

DB 6 VYLSECKTNGKXNYRGTMSTKNGITCOKWSSTSPHPRPSPATHPSEGLSENYCRNPDN 65  
QY 61 DPGPWCYTTDPKRYDYCDILECEECCHGCGENYDGKISKTMSGLBEOAMDSPHAF 120  
DB 66 DPGPWCYTTDPKRYDYCDILECEECCHGCGENYDGKISKTMSGLBEOAMDSPHAF 125  
QY 121 GYIPSKFPKXNKKYCRNPDLRPMWCTTDPNKRMECDIPRCTPPSSGPTYOCLK 180  
DB 126 GYIPSKFPKXNKKYCRNPDLRPMWCTTDPNKRMECDIPRCTPPSSGPTYOCLK 185  
QY 181 GTGENYRGNAVAVTSGHTCOHWSAOTPHHTERTPENPCKNIDENYCRNPDGKRAFWCHT 240  
DB 186 GTGENYRGNAVAVTSGHTCOHWSAOTPHHTERTPENPCKNIDENYCRNPDGKRAFWCHT 245  
QY 241 TNSQVMEYCKIPSCDSSPV 260  
DB 246 TNSQVMEYCKIPSCDSSPV 265

RESULT 13  
US-10-131-241-42  
Sequence 42, Application US/10131241  
Publication No. US20030012792A1  
GENERAL INFORMATION:  
APPLICANT: Holaday, John W.  
Fortier, Anne H.  
TITLE OF INVENTION: Compositions and Methods for Inhibiting Endothelial Cell Proliferation  
FILE REFERENCE: 05213-0344 43170-271565  
CURRENT APPLICATION NUMBER: US/10/131,241  
CURRENT FILING DATE: 2002-07-22  
PRIOR APPLICATION NUMBER: US 09/413,049  
PRIOR FILING DATE: 1999-10-06  
PRIOR APPLICATION NUMBER: US 09/316,802  
PRIOR FILING DATE: 1999-05-21  
PRIOR APPLICATION NUMBER: US 60/086,586  
PRIOR FILING DATE: 1998-05-22  
NUMBER OF SEQ ID NOS: 65  
SOFTWARE: Patentin version 3.1  
SEQ ID NO: 42  
LENGTH: 378  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-131-241-42

Query Match 99.7%; Score 1535; DB 14; Length 378;  
Best Local Similarity 99.6%; Pred. No. 7.8e-120;  
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
1 VYLSECKTNGKXNYRGTMSTKNGITCOKWSSTSPHPRPSPATHPSEGLSENYCRNPDN 60  
DB 6 VYLSECKTNGKXNYRGTMSTKNGITCOKWSSTSPHPRPSPATHPSEGLSENYCRNPDN 65  
QY 61 DPGPWCYTTDPKRYDYCDILECEECCHGCGENYDGKISKTMSGLBEOAMDSPHAF 120  
DB 66 DPGPWCYTTDPKRYDYCDILECEECCHGCGENYDGKISKTMSGLBEOAMDSPHAF 125  
QY 121 GYIPSKFPKXNKKYCRNPDLRPMWCTTDPNKRMECDIPRCTPPSSGPTYOCLK 180  
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QY 181 GTGENYRGNAVAVTSGHTCOHWSAOTPHHTERTPENPCKNIDENYCRNPDGKRAFWCHT 240  
DB 186 GTGENYRGNAVAVTSGHTCOHWSAOTPHHTERTPENPCKNIDENYCRNPDGKRAFWCHT 245  
QY 241 TNSQVMEYCKIPSCDSSPV 260  
DB 246 TNSQVMEYCKIPSCDSSPV 265

RESULT 14  
US-10-127-066-42



Sequence 42: Application US/10127066  
 Publication NO: US20030064926A1  
 GENERAL INFORMATION:  
 APPLICANT: O'Reilly, Michael S.  
 APPLICANT: Folkmann, M. Judah  
 APPLICANT: Cao, Yihai  
 APPLICANT: Sim, Kim Lee  
 TITLE OF INVENTION: Angiotensin Fragments and Method of Use  
 FILE REFERENCE: 05213-0612 43170-272529  
 CURRENT APPLICATION NUMBER: US/10/127,066  
 PRIOR FILING DATE: 2002-07-23  
 NUMBER OF SEQ ID NOS: 45  
 SOFTWARE: PatentIn version 3.1  
 SEQ ID NO: 42  
 LENGTH: 378  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-10-127-066-42

Query Match 99.7%; Score 1535; DB 14; Length 378;  
 Best Local Similarity 99.6%; Pred. No. 7.8e-120;  
 Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VYLSECKTGNGKRYRGTMSTKNGITCQKWSSTSPHRRPSPATHPSEGLEENYCRNPDN 60  
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 DB 6 VYLSECKTGNGKRYRGTMSTKNGITCQKWSSTSPHRRPSPATHPSEGLEENYCRNPDN 65  
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 QY 61 DPOGPMCTTDPPEKRYDYCDILECEECMHCSENGYDGIKSTMSGLECOAMDOSPPAH 120  
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 DB 66 DPOGPMCTTDPPEKRYDYCDILECEECMHCSENGYDGIKSTMSGLECOAMDOSPPAH 125  
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 QY 181 GTGENYRGNAVAVTSGHTCOHMSAQTPHTHERTPENPCKNLDENYCRNPDGRAPWCHT 240  
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 DB 186 GTGENYRGNAVAVTSGHTCOHMSAQTPHTHERTPENPCKNLDENYCRNPDGRAPWCHT 245  
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 QY 241 TNSQVRMEYCKIPSCDSSPV 260  
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 DB 246 TNSQVRMEYCKIPSCDSSPV 265  
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RESULT 15  
 US-10-304-287-7  
 Sequence 7: Application US/10304287  
 Publication NO: US20030083234A1  
 GENERAL INFORMATION:  
 APPLICANT: Waisman, David M.  
 APPLICANT: Kwon, Mijung  
 TITLE OF INVENTION: Anti-angiogenesis methods, compositions and uses therefor  
 FILE REFERENCE: ME02-001  
 CURRENT APPLICATION NUMBER: US/10/304,287  
 CURRENT FILING DATE: 2002-11-26  
 PRIOR APPLICATION NUMBER: US 60/333,866  
 PRIOR FILING DATE: 2001-11-28  
 NUMBER OF SEQ ID NOS: 8  
 SOFTWARE: Microsoft Word  
 SEQ ID NO: 7  
 LENGTH: 391  
 TYPE: PRT  
 ORGANISM: mammalian  
 US-10-304-287-7

Query Match 99.7%; Score 1535; DB 14; Length 391;  
 Best Local Similarity 99.6%; Pred. No. 8.1e-120;  
 Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 61 DPOGPMCTTDPPEKRYDYCDILECEECMHCSENGYDGIKSTMSGLECOAMDOSPPAH 120  
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 DB 62 DPOGPMCTTDPPEKRYDYCDILECEECMHCSENGYDGIKSTMSGLECOAMDOSPPAH 121  
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 QY 121 GYIPSKFPNKKLKKNYCRNPDRELPMWCFCTTDPNKRWELCDIPRCTTTPSSGPTYQCLK 180  
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 QY 181 GTGENYRGNAVAVTSGHTCOHMSAQTPHTHERTPENPCKNLDENYCRNPDGRAPWCHT 240  
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 DB 182 GTGENYRGNAVAVTSGHTCOHMSAQTPHTHERTPENPCKNLDENYCRNPDGRAPWCHT 241  
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 QY 241 TNSQVRMEYCKIPSCDSSPV 260  
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 DB 242 TNSQVRMEYCKIPSCDSSPV 261  
 |||||||

Search completed: July 27, 2005, 03:43:22  
 Job time : 158 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 27, 2005, 03:24:10 / Search time 16 seconds

(without alignments)  
1563.522 Million cell updates/sec

Title: US-09-502-176-2

Perfect score: 1540

Sequence: 1 VYLSECKTGNGKRYRGTMK.....TNSQVMEYCKIPSCDSPV 260

Scoring table:

BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

1: PIR 79:.\*  
2: PIR1:.\*  
3: PIR2:.\*  
4: PIR3:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1535	99.7	810	1	PLHU
2	1442	93.6	810	2	PLHU
3	1282	83.9	790	1	PLPG
4	1291	83.8	812	1	PLBO
5	1274	82.7	812	1	PLMS
6	1237	80.3	810	2	PLMS
7	881	57.2	2869	2	TI8518
8	797	51.8	728	1	UH0579
9	782	50.4	728	1	A35644
10	776.5	50.4	710	1	IS1283
11	776	50.4	728	1	A60185
12	766.5	49.8	716	1	JCS061
13	754.5	49.0	411	2	IS1285
14	753.5	48.9	716	1	A40332
15	749	48.6	4548	1	S00657
16	739	48.0	711	1	A47136
17	739	48.0	1420	2	A33869
18	505	32.8	455	2	A61545
19	499	32.4	460	2	B61545
20	391.5	25.4	336	2	B61545
21	372	24.2	625	2	TRBO
22	362.5	23.5	169	2	A40522
23	357.5	23.2	618	2	A38827
24	351	22.8	622	1	TRHU
25	348	22.6	617	2	SI0511
26	309.5	20.1	562	1	UKHUT
27	295.5	19.2	559	1	A35029
28	281.5	18.3	559	1	A29941
29	278	18.1	120	2	B61545

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30	271	17.6	89	2	A60140	plasmin (EC 3.4.21
31	268	17.4	123	2	C61545	plasmin (EC 3.4.21
32	241.5	15.7	937	2	A45082	neurotrophic recep
33	240	15.6	943	2	B45082	neurotrophic recep
34	237.5	15.4	946	1	A47299	cor-related recept
35	233	15.1	603	2	S28941	coagulation factor
36	214	13.9	558	2	JCS878	plasmin hyaluronan
37	210	13.6	560	1	UC4795	plasmin hyaluronan
38	201	13.1	291	2	I38098	t-plasminogen acti
39	198	12.9	615	1	KFHU12	coagulation factor
40	190.5	12.4	593	2	S45281	coagulation factor
41	188.5	12.2	655	1	A46680	hepatocyte growth
42	178.5	11.6	806	2	TI8840	hypothetical prote
43	165	10.7	433	1	UN0560	u-plasminogen acti
44	153	9.9	442	1	UKRG	u-plasminogen acti
45	151	9.8	432	1	S18932	u-plasminogen acti

## RESULT 1

PLHU

plasmin (EC 3.4.21.7) precursor [validated] - human  
N/Alternate names: plasminogen precursor (monomer)  
N/Contains: angiotensin, microplasmin, plasminogen  
C/Species: Homo sapiens (man)  
C/Date: 24-Apr-1984 #sequence revision 02-Dec-1994 #text change 09-Jul-2004  
C/Accession: A35229; I52242; A26646; I62738; I84609; S03735; A00929; A04627; A04625; A0-  
R/Petersen, T.E.; Martzen, M.R.; Ichinose, A.; Davie, B.W.  
J. Biol. Chem. 265: 6104-6111, 1990  
A/Title: Characterization of the gene for human plasminogen, a key proenzyme in the fibrinolytic system  
A/Reference number: A35229; MUID:90202879; PMID:2318848  
A/Accession: A35229  
A/Molecule type: DNA  
A/Residues: 1-810 <PRT>  
A/Cross-references: UNIPROT:P00747; UNIPROT:Q9UHQ9; UNIPROT:Q9UW12; GB:J05286; GB:M34276  
A/Experimental source: Leukocyte; lung fibroblast  
R/Malgaroli, N.; Bruno, L.; Pontoglio, M.; Candiani, G.; Meroni, G.; Ottolenghi, S.; Tr  
Biochem. Biophys. Res. Commun. 173: 1013-1018, 1990  
A/Title: Definition of the transcription initiation site of human plasminogen gene in 15  
A/Reference number: I52242; MUID:91097523; PMID:2268308  
A/Accession: I52242  
A/Status: translated from GB/EMBL/DBJ  
A/Molecule type: DNA  
A/Residues: 1-16 <MAL1>  
A/Cross-references: GB:M62890; NID:g190092; PIDN:AAA36454.1; PID:g553613  
R/Forstgen, M.; Raden, B.; Israelsson, M.; Larsson, K.; Heden, L.O.  
FEBS Lett. 213: 254-260, 1987  
A/Title: Molecular cloning and characterization of a full-length cDNA clone for human p1  
A/Reference number: A26646; MUID:87162490; PMID:3030813  
A/Accession: A26646  
A/Molecule type: mRNA  
A/Residues: 1-471, 'D', 473-810 <FOR>  
A/Cross-references: GB:X05199; NID:g35530; PIDN:CAA28831.1; PID:g35531  
R/Malinowski, D.P.; Sadler, J.E.; Davie, E.W.  
Biochemistry 23: 4243-4250, 1984  
A/Title: Characterization of a complementary deoxyribonucleic acid coding for human and  
A/Reference number: I45961; MUID:95023311; PMID:6148961  
A/Accession: I62738  
A/Status: translated from GB/EMBL/DBJ  
A/Molecule type: mRNA  
A/Residues: 292-471, 'D', 473-810 <MAL2>  
A/Cross-references: GB:K02922; NID:g190112; PIDN:AAA60124.1; PID:g387031  
A/Accession: I84609  
A/Status: translated from GB/EMBL/DBJ  
A/Molecule type: DNA  
A/Residues: 367-419 <MAL3>  
A/Cross-references: GB:K02921; NID:g190110; PIDN:AAA60123.1; PID:g190111  
R/Brunholz, R.A.; Lerch, P.G.; Schaller, J.; Rickli, E.E.; Legler, W.; Manneberg, M.;  
Eur. J. Biochem. 114: 465-470, 1981  
A/Title: Comparison of the primary structure of the N-terminal CNBR fragments of human,

A:Reference number: S03735; MUID:81212097; PMID:7238497  
 A:Accession: S03735  
 A:Molecule type: protein  
 A:Residues: 20-71, 'E', 73-76 <BRU>  
 R:Scitrip-Jensen, L.; Petersen, T.E.; Magnusson, S.  
 submitted to the Atlas, July 1977  
 A:Reference number: A00929  
 A:Accession: A00929  
 A:Molecule type: protein  
 A:Residues: 20-71, 'E', 73-85, 87-106, 'D', 108-360, 'E', 362-810 <SOT>  
 R:Wiman, B.  
 Eur. J. Biochem. 76, 129-137, 1977  
 A:Title: Primary structure of the B-chain of human plasmin.  
 A:Reference number: A04627; MUID:77225245; PMID:142009  
 A:Accession: A04627  
 A:Molecule type: protein  
 A:Residues: 581-810 <W11>  
 R:Wiman, B.; Wallen, P.  
 Eur. J. Biochem. 50, 489-494, 1975  
 A:Title: Structural relationship between "glutamic acid" and "lysine" forms of human pl  
 A:Reference number: A04625; MUID:75093329; PMID:122932  
 A:Accession: A04625  
 A:Molecule type: protein  
 A:Residues: 20-50, 'Q', 51-71, 'E', 73-85, 87-100 <W12>  
 R:Wiman, B.; Wallen, P.  
 Eur. J. Biochem. 58, 539-547, 1975  
 A:Title: Amino-acid sequence of the cyanogen-bromide fragment from human plasminogen th  
 A:Accession: A04626; MUID:76043692; PMID:126863  
 A:Accession: A04626  
 A:Molecule type: protein  
 A:Residues: 483-507, 'E', 509-604 <W13>  
 R:Robins, K.C.; Bernabe, P.; Arzadon, L.; Summaria, L.  
 J. Biol. Chem. 248, 1631-1633, 1973  
 A:Title: The primary structure of human plasminogen. II. The histidine loop of human pl  
 A:Reference number: A52125; MUID:73149248; PMID:4694729  
 A:Contents: annotation; active site  
 R:Groskopf, W.R.; Summaria, L.; Robbins, K.C.  
 J. Biol. Chem. 244, 3590-3597, 1969  
 A:Title: Studies on the active center of human plasmin. Partial amino acid sequence of a  
 A:Reference number: A52048; MUID:69234739; PMID:4240117  
 A:Contents: annotation; active site  
 R:Trexler, M.; Vall, Z.; Patchy, L.  
 J. Biol. Chem. 257, 7401-7406, 1982  
 A:Title: Structure of the omega-aminocarboxylic acid-binding sites of human plasminogen.  
 A:Reference number: A52382; MUID:8213905; PMID:6919539  
 A:Contents: annotation; omega-aminocarboxylic acid binding sites  
 R:Vall, Z.; Patchy, L.  
 J. Biol. Chem. 259, 13690-13694, 1984  
 A:Title: The fibrin-binding site of human plasminogen. Arginines 32 and 34 are essential  
 A:Reference number: A52458; MUID:85054794; PMID:6094526  
 A:Contents: annotation; fibrin binding site; omega-aminocarboxylic acid binding site  
 R:Go, Y.; Ji, R.W.; Davidson, D.; Schaller, J.; Marti, D.; Seehndel, S.; McCance, S.G.;  
 J. Biol. Chem. 271, 29461-29467, 1996  
 A:Title: Kringle domains of human angiotensin. Characterization of the anti-proliferativ  
 A:Reference number: A58811; MUID:97067211; PMID:8910613  
 A:Contents: annotation  
 R:Liljen, H.R.; Uemu, F.; Bini, A.; Collen, D.  
 Biochemistry 37, 4699-4702, 1998  
 A:Title: Generation of an angiotensin-like fragment from plasminogen by streptolysin-1 (W  
 A:Reference number: A58812; MUID:9548733; PMID:9548733  
 A:Contents: annotation  
 R:Tulinsky, A.; Mulichak, A.M.  
 submitted to the Brookhaven Protein Data Bank, July 1991  
 A:Reference number: A51341; PDB:1PK4  
 A:Contents: annotation; X-ray crystallography, 1.9 angstroms, residues 376-454  
 R:Tulinsky, A.; Wu, T.P.  
 submitted to the Brookhaven Protein Data Bank, July 1991  
 A:Reference number: A51488; PDB:2PK4  
 A:Contents: annotation; X-ray crystallography, 2.25 angstroms, residues 375-454  
 R:Wu, T.P.; Tulinsky, A.  
 submitted to the Brookhaven Protein Data Bank, August 1993  
 A:Reference number: A51911; PDB:1PKR

A:Contents: annotation; X-ray crystallography, 2.48 angstroms, residues 102-181  
 R:Padmanabhan, K.; Tulinsky, A.  
 submitted to the Brookhaven Protein Data Bank, April 1994  
 A:Reference number: A52408; PDB:1PKM  
 A:Contents: annotation; X-ray crystallography, 2.25 angstroms, residues 377-454  
 R:Tulinsky, A.; Mathews, I.I.  
 submitted to the Brookhaven Protein Data Bank, December 1995  
 A:Reference number: A55244; PDB:1CEA  
 A:Contents: annotation; X-ray crystallography, 2.1 angstroms, residues 102-181  
 R:Tulinsky, A.; Mathews, I.I.  
 submitted to the Brookhaven Protein Data Bank, December 1995  
 A:Reference number: A55245; PDB:1CEB  
 A:Contents: annotation; X-ray crystallography, 2.1 angstroms, residues 102-181  
 R:Mulichak, A.M.; Tulinsky, A.; Ravichandran, K.G.  
 Biochemistry 30, 10576-10588, 1991  
 A:Title: Crystal and molecular structure of human plasminogen kringle 4 refined at 1.9 /  
 A:Reference number: A58819; MUID:92031502; PMID:1657148  
 A:Contents: annotation  
 R:Wu, T.P.; Padmanabhan, K.; Tulinsky, A.; Mulichak, A.M.  
 Biochemistry 30, 10589-10594, 1991  
 A:Title: The refined structure of the epsilon-aminocaproic acid complex of human plasm  
 A:Reference number: A58818; MUID:92031503; PMID:1657149  
 A:Contents: annotation  
 R:de Vos, A.M.; Utlech, M.H.; Kelley, R.F.; Padmanabhan, K.; Tulinsky, A.; Westbrook, M  
 Biochemistry 31, 270-279, 1992  
 A:Title: Crystal structure of the kringle 2 domain of tissue plasminogen activator at 2  
 A:Reference number: A39483; MUID:92118803; PMID:1310033  
 A:Contents: annotation; X-ray crystallography, 2.4 angstroms  
 R:Sec, B.; Teeter, M.M.; Whitlow, M.; Yamano, A.  
 submitted to the Brookhaven Protein Data Bank, June 1995  
 A:Reference number: A65980; PDB:1KRN  
 A:Contents: annotation; X-ray crystallography, 1.67 angstroms, residues 376-454  
 R:Rejzante, M.; Llinas, M.  
 submitted to the Brookhaven Protein Data Bank, August 1996  
 A:Reference number: A65803; PDB:1HPU  
 A:Contents: annotation; conformation by (1)H-NMR, residues 103-181  
 R:Rejzante, M.; Llinas, M.  
 submitted to the Brookhaven Protein Data Bank, August 1996  
 A:Reference number: A65804; PDB:1HPK  
 A:Contents: annotation; conformation by (1)H-NMR, residues 103-181  
 R:Rejzante, M.R.; Llinas, M.  
 Eur. J. Biochem. 221, 927-937, 1994  
 A:Title: Solution structure of the epsilon-aminohexanoic acid complex of human plasmin  
 A:Reference number: A58817; MUID:94237158; PMID:8181476  
 A:Contents: annotation; conformation by (1)H-NMR  
 C:Comment: plasminogen is synthesized by the kidney and is present in plasma and many o  
 C:Comment: plasminogen is converted to plasmin by plasminogen activators (see PIR:UGHU  
 C:PIR:FGHGB)  
 C:Comment: Plasmin is inactivated by alpha-2-antiplasmin (see PIR:ITHUA2) immediately a  
 rg-580, resulting in two chains connected by two disulfide bonds. Without the inhibitor  
 C:Comment: Microplasmin is formed by autolytic cleavage of plasmin under artificial con  
 C:Comment: Streptolysin 1 (see PIR:KCHUS1) acts on plasminogen to produce angiotensin. T  
 ting solid tumors.  
 C:Genetics:  
 A:Gene: GDB:PLG  
 A:Cross-references: GDB:119498; OMIM:173350  
 A:Map position: 6q26-6q27  
 A:Intons: 17/1, 62/2, 98/1, 136/2, 183/1, 223/2, 263/1, 317/2, 366/1, 419/2, 480/1, 552  
 C:Function:  
 A:Description: dissolves the fibrin of blood clots; acts as a proteolytic factor in a v  
 ns the walls of the graafian follicle; also activates the urokinase-type plasminogen ac  
 C:Pathway: fibrinolysis  
 C:Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homolog  
 C:Keywords: angogenesis inhibitor; blood; duplication; fibrinolysis; glycoprotein; hyd  
 F:1-96/Domain: plasminogen-related protein precursor homology <PLRH>  
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 F:20-810/Product: plasminogen #status experimental <PRO>  
 F:20-96/Domain: activation peptide #status experimental <APN>

F.7/9-466/Product: angiostratin [status experimental] <AST>  
F.9/7-580, 581-810/Product: plasmin [status experimental] <MT>  
F.9/7-580/Domain: plasmin chain A [status experimental] <CHA>  
F.103-181/Domain: kringle homology <K1>  
F.185-263/Domain: kringle homology <K2>  
F.1275-325/Domain: kringle homology <K3>  
F.3377-456/Domain: kringle homology <K4>  
F.481-560/Domain: kringle homology <K5>  
F.7550-580, 581-810/Product: micropotasmin [status experimental] <MPT>

Query Match	99.7%	Score 1535;	DB 1;	Length 810;
Best Local Similarity	99.6%	Pred. No. 5.6e-104;		
Matches 259; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;

QY	158	VYLSSECKTNGKNGYRGTMSKTKNGITCQKMSSTSPHRAFPSPATHPSGLEBNYCRPN	60
Db	98	VYLSSECKTNGKNGYRGTMSKTKNGITCQKMSSTSPHRAFPSPATHPSGLEBNYCRPN	15
QY	61	DPOPMYCTTDPPEKRYDCDILIECEBCHCSEENDGKITSTMGLCQAMDSOPH	120
Db	158	DPOPMYCTTDPPEKRYDCDILIECEBCHCSEENDGKITSTMGLCQAMDSOPH	21
QY	121	GYPKPEPNLKKNYCRNPDELRPMCFETTPDNKWEKCDIPRCTPSPSGPTOCLK	180
Db	218	GYPKPEPNLKKNYCRNPDELRPMCFETTPDNKWEKCDIPRCTPSPSGPTOCLK	27
QY	181	GTGENTRGNAVTVSGHTCQHMSAQTPHTHERTPENFPCNKIDENYCANPDGKAPWCHT	240
Db	278	GTGENTRGNAVTVSGHTCQHMSAQTPHTHERTPENFPCNKIDENYCANPDGKAPWCHT	33
QY	241	TNSOVRWEYCKIPSCDSSPV 260	
Db	338	TNSOVRWEYCKIPSCDSSPV 357	

RESULT 2  
P30049

Plasmin (EC 3.4.21.7) precursor - rheus macaque  
 C:Species: Macaca mulatta (rheus macaque)  
 C>Date: 31-Mar-1989 #sequence\_revision 31-Mar-1989 #text\_change 09-Jul-2004  
 C:Accession: B32869; B30848  
 R:Tomlinson, J.E.; McLean, J.W.; Lawn, R.M.  
 J. Biol. Chem. 264, 5957-5965, 1989  
 A:Title: Rhesus monkey apolipoprotein(a). Sequence, evolution, and sites of synthesis.  
 A:Reference number: A32869; MUID:89174660; PMID:2925643  
 A:Accession: B32869  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-810 <TOM>  
 A:Cross-references: UNIPROT:P12545; GB:J04697; NID:G342272; PIDN:AAA36901.1; PID:G342272  
 C:Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homology  
 C:Keywords: fibrinolysis; glycoprotein; hydrolase; kringle; serine proteinase  
 F:1-96/Domain: plasminogen-related protein precursor homology <PLPH>  
 F:1-9/Domain: signal sequence #status predicted <SIG>  
 F:103-181/Domain: kringle homology <KR1>  
 F:185-262/Domain: kringle homology <KR2>  
 F:275-352/Domain: kringle homology <KR3>  
 F:377-454/Domain: kringle homology <KR4>  
 F:481-560/Domain: kringle homology <KR5>  
 F:581-803/Domain: trypsin homology <TRY>  
 F:48-73, 53-61, 103-181, 124-164, 152-176, 185-262, 188-316, 206-245, 234-257, 275-352, 296-335, 320-365, 665-760/Active site: His, Asp, Ser #status predicted  
 F:622,665,760/Active site: His, Asp, Ser #status predicted

Query Match	93.6%	Score 1442	DB 2	length 810
Best Local Similarity	93.1%	Pred. No. 3	le-97	
Matches 242	Conservative 9	Mismatches 9	Incls 0	Gaps 0
QY	1	VTLSSECTGNGKRYRCSTMTKNGITCCOMMSSTSPRRPFSATPHPSGTELEANTCRNPDN	60	
DB	98	VTLSSECTGNGKNGKRGMSKTRIGITCCOMMSSTSPRRPFSATPHPSGTELEANTCRNPDN	157	
QY	61	DPGGPMVCTTDPKRYDYCDILECEECHMGSGENYDKISKNTSGLECCOMMSQSPHAR	120	

Db 158 DGGGPGCYTTDBERPFIDCIPECEDECMGSGENYOGKISKTNISGLECOAMDSQHPAH 217  
 Qy 121 GYIPSKFPMKNLKKNYCENPDELPLMCFETTDPMKRMELCDI PRCTTPPESSGPTYOCLK 180  
 Db 218 GYIPSKFPMKNLKKNYCENPDELPLMCFETTDPMKRMELCDI PRCTTPPESSGPTYOCLK 277  
 Qy 181 GIGENYRGVAVTVBSGHTCOHWSAQTPTHTERTPENFPCKMLDENTYCRNPDGKAPWCHT 240  
 Db 278 GIGENYRGVAVTVBSGHTCHGWSAQTPTHTNRTPENFPCKMLDENTYCRNPDGEAPWCYT 337  
 Qy 241 TNSQVMEYCKIIPSCDSSPV 260  
 Db 338 TNSQVMEYCKIIPSCDSSPV 357

### RESULT 3

Plasmin (EC 3.4.21.7) precursor - pig (fragment)  
 N/Alternate names: plasminogen  
 N/Contains: miniplasminogen  
 C/Species: Sus scrofa domestica (domestic pig)  
 C/Date: 07-Sep-1990 #sequence, revision 01-Nov-1996 #text\_change 09-Jul-2004  
 C/Accession: S03733, S03737, A25834  
 R/Schaller, J.; Marti, T.; Roessellet, S.J.; Kaempfer, U.; Rickli, E.E.  
 Fibrinolytics 1, 91-102, 1987  
 A/Title: Amino acid sequence of the heavy chain of porcine plasmin. Comparison of the c  
 A/Reference number: S03733  
 A/Accession: S03733  
 A/Molecule type: protein  
 A/Residues: 1-560 <SCH>  
 A/Cross-references: UNIPROT:P06867  
 R/Brunsholz, R.A.; Lerch, P.G.; Schaller, J.; Rickli, E.E.; Lergier, W.; Manneberg, M.  
 Eur. J. Biochem. 114, 465-470, 1981  
 A/Title: Comparison of the primary structure of the N-terminal CNBR fragments of human,  
 A/Reference number: S03735; PMID:81212097; PMID:7238497  
 A/Accession: S03737  
 A/Molecule type: protein  
 A/Residues: 1-57 <BRU>  
 R/Marti, T.; Schaller, J.; Rickli, E.E.  
 Eur. J. Biochem. 149, 279-285, 1985  
 A/Title: Determination of the complete amino-acid sequence of porcine miniplasminogen.  
 A/Reference number: A25834; PMID:85203907; PMID:3846533  
 A/Accession: A25834  
 A/Molecule type: protein  
 A/Residues: 450-790 <MAR>  
 C/Function:  
 A:Description: dissolves the fibrin of blood clots; acts as a proteolytic factor in a v  
 ns the walls of the graafian follicle; also activates the urokinase-type plasminogen ac  
 A/Pathway: fibrinolysis  
 C/Superfamily: plasmin; kringlike homology; plasminogen-related protein precursor homology  
 C/Keywords: fibrinolysis; glycoprotein; hydrolase; kidney; kringlike; plasma; serine prote  
 F:1-790/Product: plasminogen #status predicted <PO>  
 F:1-77/Domain: plasminogen-related protein precursor homology (fragment) <PLPH>  
 F:1-77/Domain: activation peptide #status predicted <AP>  
 F:78-560/Product: plasmin chain A #status predicted <ACH>  
 F:84-162/Domain: kringlike homology <KR1>  
 F:166-243/Domain: kringlike homology <KR2>  
 F:256-333/Domain: kringlike homology <KR3>  
 F:358-435/Domain: kringlike homology <KR4>  
 F:450-790/Product: miniplasminogen #status experimental <MIN>  
 F:461-540/Domain: kringlike homology <KR5>  
 F:561-790/Product: plasmin chain B #status experimental <BCH>  
 F:561-783/Domain: trypsin homology <TRY>  
 F:30-54,34-42,84-162,105-145,133-157,166-243,169-297,187-226,215-238,256-333,277-316,300  
 bonds: #status predicted  
 F:602,645,740/Active site: His, Asp, Ser #status predicted

Query Match	83.9%	Score 1292	DB 1	Length 790
Best Local Similarity	81.4%	Pred. No. 2,4e-66		
Matches 210	Conservative 23	Mismatches 25	Indels 0	Gaps 0

F;110-188/Domain: kringle homology &lt;KR1&gt;

A; Pathway: fibrinolysis

C; Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homology

C/Keywords: angiogenesis inhibitor; blood; duplication; fibrinolysis; glycoprotein; hyd  
 F:1-96/Domain: plasminogen-related protein precursor homology <PLPH>  
 F:1-19/Domain: signal sequence #status predicted <SIG>  
 F:20-812/Product: plasminogen #status predicted <PRO>  
 F:20-96/Domain: activation peptide #status predicted <APT>  
 F:79-466/Product: angiotensin #status predicted <AST>  
 F:79-581,582-812/Product: plasmin #status predicted <WAT>  
 F:97-581/Domain: chain A #status predicted <ACH>  
 F:103-181/Domain: kringles homology <KR1>  
 F:185-262/Domain: kringles homology <KR2>  
 F:275-352/Domain: kringles homology <KR3>  
 F:377-454/Domain: kringles homology <KR4>  
 F:481-560/Domain: kringles homology <KR5>  
 F:582-812/Domain: chain B #status predicted <BCH>  
 F:582-805/Domain: trypsin homology <TRY>  
 F:59-73,55-61,103-161,124-164,152-176,185-262,188-316,206-245,224-257,275-352,296-335,32  
 F:59-73,55-61,103-161,124-164,152-176,185-262,188-316,206-245,224-257,275-352,296-335,32  
 Bonds: #status predicted  
 F:78-79/Cleavage site: Glu-Asn (stromelysin 1) #status predicted  
 F:136-308/Binding site: carboxylate (Asn) (covalent) #status predicted  
 F:466-467/Cleavage site: Thr-Val (stromelysin 1) #status predicted  
 F:581-582/Cleavage site: Arg-Val (plasminogen activator) #status experimental  
 F:624,667,762/Active site: His, Asp, Ser #status predicted

Query Match 82.7%; Score 1274; DB 1; Length 812;  
 Best Local Similarity 80.6%; Pred. No. 4,9e-85;  
 Matches 208; Conservative 22; Mismatches 28; Indels 0; Gaps 0;

QY 1 VLSECKTGNKNGKNTGMSKTNGITCQKMSSTSPRRPRESPATHPSEGLEENYCRNPND 60  
 DB 98 VLSECKTGNKNGKNTGMSKTNGITCQKMSSTSPRRPRESPATHPSEGLEENYCRNPND 157  
 QY 61 DQGPWCYTTDPKRYDYCDILECEBCHGSGENYDCKISKTMSGLCQAWDSQSPHAF 120  
 DB 158 DQGPWCYTTDPKRYDYCDILECEBCHGSGENYDCKISKTMSGLCQAWDSQSPHAF 217  
 QY 121 GYIPSEFPNKLKKNYCRNPDELRPMCFITTDNPKRMELCDIPRCTTPPSGPTQCLK 180  
 DB 218 GYIPSEFPNKLKKNYCRNPDELRPMCFITTDNPKRMELCDIPRCTTPPSGPTQCLK 277  
 QY 181 GTGENYRGNVAVTSGHTCOHMSAQTPTHTERTPENPCNDLDENYCRNPDKRAFWCHT 240  
 DB 278 GTGENYRGNVAVTSGHTCOHMSAQTPTHTERTPENPCNDLDENYCRNPDKRAFWCHT 337  
 QY 241 TNSQVRMEYCKIPSCDS 258  
 DB 338 TDSQVRMEYCKIPSCDS 355

RESULT 6  
 146260  
 Plasmin (EC 3.4.21.7) precursor - western European hedgehog  
 C/Species: Echinacea europaea (western European hedgehog)  
 C/Date: 21-Feb-1997 #sequence\_revision 21-Feb-1997 #text\_change 09-Jul-2004  
 C/Accession: 146260  
 R/Law, R.M.; Boommark, N.W.; Schwartz, K.; Lindahl, G.E.; Wade, D.P.; Byrne, C.D.; Fong  
 J. Biol. Chem. 270, 24004-24009, 1995  
 A/Title: The recurring evolution of lp(a): Insights from cloning of hedgehog apolipoprotein  
 A/Reference number: 146259; PMID:96025778; PMID:7592597  
 A/Accession: 146260  
 A/Status: preliminary; translated from GB/EMBL/DBJ  
 A/Molecule type: mRNA  
 A/Residues: 1-810 <LAW>  
 A/Cross-references: UNIPROT:Q29485; EMBL:U33171; NID:G1046360; PID:G1046361  
 C/Suprafamily: Plasmin; kringles homology; plasminogen-related protein precursor homology  
 C/Keywords: hydrolase; serine proteinase  
 F:1-96/Domain: plasminogen-related protein precursor homology <PLPH>  
 F:103-181/Domain: kringles homology <KR1>  
 F:185-262/Domain: kringles homology <KR2>  
 F:275-352/Domain: kringles homology <KR3>  
 F:377-454/Domain: kringles homology <KR4>  
 F:481-561/Domain: kringles homology <KR5>  
 F:582-803/Domain: trypsin homology <TRY>

Query Match 80.3%; Score 1237; DB 2; Length 810;  
 Best Local Similarity 77.9%; Pred. No. 2.4e-82;  
 Matches 201; Conservative 26; Mismatches 31; Indels 0; Gaps 0;

QY 1 VLSECKTGNKNGKNTGMSKTNGITCQKMSSTSPRRPRESPATHPSEGLEENYCRNPND 60  
 DB 98 VLSECKTGNKNGKNTGMSKTNGITCQKMSSTSPRRPRESPATHPSEGLEENYCRNPND 157  
 QY 61 DQGPWCYTTDPKRYDYCDILECEBCHGSGENYDCKISKTMSGLCQAWDSQSPHAF 120  
 DB 158 DQGPWCYTTDPKRYDYCDILECEBCHGSGENYDCKISKTMSGLCQAWDSQSPHAF 217  
 QY 121 GYIPSEFPNKLKKNYCRNPDELRPMCFITTDNPKRMELCDIPRCTTPPSGPTQCLK 180  
 DB 218 GYIPSEFPNKLKKNYCRNPDELRPMCFITTDNPKRMELCDIPRCTTPPSGPTQCLK 277  
 QY 181 GTGENYRGNVAVTSGHTCOHMSAQTPTHTERTPENPCNDLDENYCRNPDKRAFWCHT 240  
 DB 278 GTGENYRGNVAVTSGHTCOHMSAQTPTHTERTPENPCNDLDENYCRNPDKRAFWCHT 337  
 QY 241 TNSQVRMEYCKIPSCDS 258  
 DB 338 TNSQVRMEYCKIPSCDS 355

RESULT 7  
 118518  
 apolipoprotein(a) - western European hedgehog (fragment)  
 C/Species: Echinacea europaea (western European hedgehog)  
 C/Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
 C/Accession: T18518  
 R/Law, R.M.; Boommark, N.W.; Schwartz, K.; Lindahl, G.E.; Wade, D.P.; Byrne, C.D.; Fong  
 J. Biol. Chem. 270, 24004-24009, 1995  
 A/Title: The recurring evolution of lp(a): Insights from cloning of hedgehog apolipoprotein  
 A/Reference number: 146259; PMID:96025778; PMID:7592597  
 A/Accession: T18518  
 A/Status: preliminary; translated from GB/EMBL/DBJ  
 A/Molecule type: mRNA  
 A/Residues: 1-2869 <LAW>  
 A/Cross-references: UNIPROT:Q28398; EMBL:U33170; NID:G1046358; PID:G1046359; PIDN:AA048;  
 C/Comment: The lipoprotein lp(a), a major inherited risk factor for atherosclerosis, coi  
 ent apolipoprotein(a).

Query Match 57.2%; Score 881; DB 2; Length 2869;  
 Best Local Similarity 55.0%; Pred. No. 5.6e-56;  
 Matches 149; Conservative 36; Mismatches 70; Indels 16; Gaps 3;

QY 3 LSECKTGNKNGKNTGMSKTNGITCQKMSSTSPRRPRESPATHPSEGLEENYCRNPNDP 62  
 DB 2495 VDCLEGTGENYRGNMAVTASGHTCQWRBESPHSHRTPTENYPTKLVGNVGNPNDE - 2553  
 QY 63 DQGPWCYTTDPKRYDYCDILECEBCHGSGENYDCKISKTMSGLCQAWDSQSPHAF 110  
 DB 2554 VAPWCYTTNSAMREYCSIPACESPTPTHTLVVPEQCLBNGENYGNMAVTASGQPCQ 2613  
 QY 111 AMDQSPHAFHGYISKEFPNKLKKNYCRNPDELRPMCFITTDNPKRMELCDIPRCTTPP 170  
 DB 2614 GMRKQTHRYHTENTPNSKLPNGYCRNPDELRPMCFITTDNPKRMELCDIPRCTTPP 2673  
 QY 171 SSGPTV---OCLKGTGENYRGNVAVTSGHTCOHMSAQTPTHTERTPENPCNDLDENYC 227  
 DB 2674 PTEPMITPDQLEGTGENYRGNVAVTSGHTCQWRBESPHSHRTPTENYPTKLVGNVGNPNDE 2733  
 QY 228 RNPQKAPNCHTNSQVRMEYCKIPSCDS 258  
 DB 2734 RNPQKAPNCHTNSQVRMEYCKIPSCDS 2764

RESULT 8  
 CH0579  
 hepatocyte growth factor precursor [validated] - human  
 N/Alternate names: hepatoleitin A; scatter factor

C:Species: Homo sapiens (man)  
C:Date: 17-Aug-1992 #sequence revision 17-Aug-1992 #text\_change 09-Jul-2004  
C:Accession: JH0579; J00333; A41140; B36677; A36577; A35512; A39006; PH0114; A37796; S001  
R:Seiki, T.; Hagiya, M.; Shimomishi, M.; Nakamura, T.; Shimizu, S.  
Gene 102, 213-219, 1991  
A:Title: Organization of the human hepatocyte growth factor-encoding gene.  
A:Reference number: JH0579; MUID:91340155; PMID:1831432  
A:Accession: JH0579  
A:Molecule type: DNA  
A:Residues: 1-728 <SE3>  
A:Cross-references: UNIPROT:P14210; DBJ:D90318  
A>Note: the authors translated the codon GAA for residue 662 as Gly  
R:Seiki, T.; Hagiya, M.; Shimomishi, M.; Nakamura, T.; Shimizu, S.  
submitted to JFID, March 1991  
A:Description: Organization of the human hepatocyte growth factor-encoding gene.  
A:Reference number: J00333  
A:Accession: J00333  
A:Molecule type: DNA  
A:Residues: 1-481,'RT',484-728 <SE2>  
R:Weidner, K.M.; Arakaki, N.; Hartmann, G.; Vandekerckhove, J.; Weingart, S.; Rieder, H.  
Proc. Natl. Acad. Sci. U.S.A. 88, 7001-7005, 1991  
A:Title: Evidence for the identity of human scatter factor and human hepatocyte growth factor  
A:Reference number: A41140; MUID:91334393; PMID:1831266  
A:Accession: A41140  
A:Molecule type: mRNA  
A:Residues: 1-728 <WE1>  
A:Cross-references: GB:M73239; NID:G337935; PIDN:AAA64239.1; PID:G337936  
R:Seiki, T.; Ihara, I.; Sugimura, A.; Shimomishi, M.; Nishikawa, T.; Asami, O.; Hagiya, M.  
Biochem. Biophys. Res. Commun. 172, 321-327, 1990  
A:Title: Isolation and expression of cDNA for different forms of hepatocyte growth factor  
A:Reference number: A36677; MUID:91025062; PMID:2145836  
A:Accession: B36677  
A:Molecule type: mRNA  
A:Residues: 1-728 <SE3>  
A:Cross-references: GB:M60718; NID:G184031; PIDN:AAA52648.1; PID:G184032  
A:Accession: A36677  
A:Molecule type: mRNA  
A:Residues: 1-161,167-728 <SE4>  
A:Cross-references: EMBL:X16323  
A:Experimental source: leukocyte  
R:Miyazawa, K.; Tsubouchi, H.; Naka, D.; Takahashi, K.; Ohtsaki, M.; Arakaki, N.; Nakaya  
Biochem. Biophys. Res. Commun. 163, 967-973, 1989  
A:Title: Molecular cloning and sequence analysis of cDNA for human hepatocyte growth factor  
A:Reference number: A35512; MUID:89392017; PMID:2528952  
A:Accession: A35512  
A:Status: not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 1-728 <MTY>  
A:Cross-references: GB:M29145; NID:G184041; PIDN:AAA52650.1; PID:G306846  
R:Rudin, J.S.; Chan, A.M.L.; Botelho, D.P.; Burgess, W.H.; Taylor, W.G.; Czech, A.C.; Hitz  
Proc. Natl. Acad. Sci. U.S.A. 88, 415-419, 1991  
A:Title: A broad-spectrum human lung fibroblast-derived mitogen is a variant of hepatocyte  
A:Reference number: A39006; MUID:91110540; PMID:1824873  
A:Accession: A39006  
A:Molecule type: mRNA  
A:Residues: 1-161,167-728 <RUB>  
A:Cross-references: GB:M55379  
A:Experimental source: embryonic lung  
R:Yoshiyama, Y.; Arakaki, N.; Naka, D.; Takahashi, K.; Hirono, S.; Kondo, J.; Nakayama,  
Biochem. Biophys. Res. Commun. 175, 660-667, 1991  
A:Title: Identification of the N-terminal residue of the heavy chain of both native and  
A:Reference number: PH0114; MUID:91207365; PMID:1826837  
A:Accession: PH0114  
A:Molecule type: protein  
A:Residues: 32-43;53-58 <YOS>  
A:Experimental source: plasma  
R:Weidner, K.M.; Behrens, J.; Vandekerckhove, J.; Birchemier, W.  
J. Cell Biol. 111, 2097-2108, 1990  
A:Title: Scatter factor: molecular characteristics and effect on the invasiveness of ep  
A:Reference number: A37796; MUID:91035621; PMID:2146276  
A:Accession: A37796  
A:Molecule type: protein  
A:Residues: 86-91;1329-344;356-363,'XX',366-370;425-434;442-447,'X',449-450;543-546,'X',5

R:Nakamura, T.; Nishizawa, T.; Hagiya, M.; Seki, T.; Shimoniishi, M.; Sugimura, A.; Tesh  
Native 342, 440-443, 1989  
A:Title: Molecular cloning and expression of human hepatocyte growth factor.  
A:Reference number: S06794; MUID:90066676; PMID:2531289  
A:Accession: S06794  
A:Molecule type: mRNA  
A:Residues: 1-31, 'HK', 34-77, 'N', 79-292, 'V', 294-299, 'W', 301-316, 'A', 318-335, 'K', 337-386,  
A:Cross-references: EMBL:X16323; NID:932081; PIDN:CAA34387.1; PID:932082  
A:Experimental source: liver  
A:Note: the authors translated the codon CAG for residue 727 as Glu  
R:Hartmann, G.; Meldini, L.; Weidner, K.M.; Sachs, M.; Vigna, E.; Comoglio, P.M.; Birch  
Proc. Natl. Acad. Sci. U.S.A. 89, 11574-11578, 1992  
A:Title: A functional domain in the heavy chain of scatter factor/hepatocyte growth fac  
A:Reference number: I59214; MUID:93087571; PMID:1280830  
A:Accession: I59214  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-288, 'ET' <HAR>  
A:Cross-references: GB:U02911; NID:9184033; PIDN:AAA52649.1; PID:9184034  
R: Miyazawa, K.; Kitamura, A.; Naka, D.; Kitamura, N.  
Eur. J. Biochem. 197, 15-22, 1991  
A:Title: An alternatively processed mRNA generated from human hepatocyte growth factor  
A:Reference number: S15443; MUID:91200041; PMID:1826653  
A:Accession: S15443  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-288, 'ET' <MY2>  
A:Cross-references: EMBL:X5574; NID:932083; PIDN:CAA0802.1; PID:932084  
R:Shima, N.; Nagao, M.; Ogaki, F.; Tsuda, E.; Murakami, A.; Higashio, K.  
Biochem. Biophys. Res. Commun. 180, 1151-1158, 1991  
A:Title: Tumor cytotoxic factor/hepatocyte growth factor from human fibroblasts: clonin  
A:Reference number: I52253; MUID:92062058; PMID:1835383  
A:Accession: I52253  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 161-166 <SH1>  
A:Cross-references: GB:S62561; NID:9237996; PIDN:AAB20169.1; PID:9237997  
C:Genetics:  
A:Gene: GDB:HGF  
A:Cross-references: GDB:127524; OMIM:142409  
A:Map position: 7q21.1-7q21.1  
A:Introns: 30/1; 85/2; 123/1; 161/2; 209/1; 249/2; 289/1; 347/2; 390/1; 424/2; 469/1; 4  
C:Complex: disulfide-bonded heterodimer of chains derived from the same precursor  
C:Function:  
A:Description: stimulates mitosis of hepatocytes and other cells  
A:Note: does not have proteinase activity  
C:Superfamily: hepatocyte growth factor/macrophage stimulating protein 1; kringle homol  
C:Keywords: alternative splicing; glycoprotein; growth factor; heterodimer; kringle; py  
F:1-31/Domin: signal sequence #status predicted <IG>  
F:32-494/495-728/Product: hepatocyte growth factor #status experimental <MAT>  
F:32-494/Domin: alpha chain #status experimental <ACH>  
F:128-206/Domin: kringle homology <K1>  
F:211-288/Domin: kringle homology <KR2>  
F:305-383/Domin: kringle homology <KR3>  
F:391-469/Domin: kringle homology <KR4>  
F:495-728/Domin: beta chain #status experimental <BCH>  
F:495-716/Domin: trypsin homology <TRY>  
F:32/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experime  
F:294,402,566,653/Binding site: carbonyl (Asn) (covalent) #status predicted  
F:487-604/Disulfide bonds: #status predicted

Query Match 51.8%; Score 797; DB 1; Length 728;  
Best Local Similarity 51.0%; Pred. No. 1,88-50;  
Matches 134; Conservative 42; Mismatches 81; Indels 6; Gaps 4;

OY 2 YLSECKTGNGKNYRGNTSKTKNGITCQKMSSTSPHRPRSPATHPSGLEBENYCRNPND 61  
DB 124 YIRNCITIGKRSYKGTYSITKSGIKCPMWSMIPHEHSFLPSSYRGDLOENYCRNPGE 183  
62 POGWCWCTTDEKRYDCDILCEE-BCMHCSGENYNGKISKMTSGLECAWDSOSPAH 120  
184 EGGWCWCTSPENRYVECDIPQCEVEWCMTCNGSYGLMDHDSGKICQAWDHQTPHRH 243



QY 121 GYIPSPKPNKLNKKYCNRPDRRLRPWCFTTDPKRWELCDIPRC--TTPPSSGP--TY 176  
 DB 244 KFLPERIPDGFPDNDYCRNPDGQGRPMVCYTLDPHTREYCAIKTCADNTMNDVPLETT 303  
 QY 177 QCLKGTGENYRGNAVAVTSQHTCOHWSAQTPHTERTPENPCKNLDENYCRNPDGRAP 236  
 DB 304 ECIQGGEGYRGVNTIWMGIPCORWDSQYPRHEDHTPENFKCKDLRENYCRNPDGSESP 363  
 QY 237 WCHTNSQVWMEYC-KIPSCDSS 258  
 DB 364 WCFTTDPNIRVGYCSQIPKCDMS 386

## RESULT 9

A35644  
 hepatocyte growth factor precursor - rat  
 N/Alternate names: hepatoinetin A; scatter factor  
 C/Species: Rattus norvegicus (Norway rat)  
 C/Date: 28-Sep-1990 #sequence\_revision 18-Nov-1992 #text\_change 09-Jul-2004  
 C/Accession: A35644; S13211  
 R/Tashiro, K.; Hagiya, M.; Nishizawa, T.; Seki, T.; Shimomishi, M.; Shimizu, S.; Nakamura  
 Proc. Natl. Acad. Sci. U.S.A. 87, 3200-3204, 1990  
 A/Title: Deduced primary structure of rat hepatocyte growth factor and expression of the  
 A/Reference number: A35644; MUID:90222197; PMID:2139229  
 A/Accession: A35644  
 A/Status: preliminary  
 A/Molecule type: mRNA  
 A/Residues: 1-728 <OKA>  
 A/Cross-references: UNIPROT:P17945; GB:D90102; GB:M32987; NID:q220766; PIDN:BA14133.1;  
 A/Note: the authors translated the codon GAG for residue 70 as Gln, GAC for residue 417  
 R/Okajima, A.; Miyazawa, K.; Kitamura, N.  
 Eur. J. Biochem. 193, 375-381, 1990  
 A/Title: Primary structure of rat hepatocyte growth factor and induction of its mRNA dur  
 A/Reference number: S13211; MUID:91031482; PMID:2146117  
 A/Accession: S13211  
 A/Status: preliminary  
 A/Molecule type: mRNA  
 A/Residues: 1-728 <OKA>  
 A/Cross-references: EMBL:X54400; NID:956353; PIDN:CAA38266.1; PID:94539554  
 C/Complex: disulfide-bonded heterodimer of chains derived from the same precursor  
 C/Function:  
 A/Description: stimulates mitosis of hepatocytes and other cells  
 A/Note: does not have proteinase activity  
 C/Superfamily: hepatocyte growth factor/macrocyte stimulating protein 1; kringe homolo  
 C/Keywords: alternative splicing; glycoprotein; growth factor; heterodimer; kringe; pyr  
 F.1-3/Domain: signal sequence #status predicted <SIG>  
 F.56-495/Domain: hepatocyte growth factor #status predicted <MAT>  
 F.56-495/Domain: hepatocyte growth factor alpha chain #status predicted <ACH>  
 F.129-207/Domain: kringe homology <KR1>  
 F.212-289/Domain: kringe homology <KR2>  
 F.306-384/Domain: kringe homology <KR3>  
 F.392-470/Domain: kringe homology <KR4>  
 F.496-728/Domain: hepatocyte growth factor beta chain #status predicted <BCH>  
 F.496-719/Domain: trypsin homology <TRY>  
 F.53/Modified site: pyroliidone carboxylic acid (Gln) (in mature form) #status predicted  
 F.52/56/Binding site: carbohydrate (Asn) (covalent) #status predicted  
 F.488-607/Disulfide bonds: #status predicted

Query Match 50.8%; Score 782; DB 1; Length 728;  
 Best Local Similarity 49.8%; Pred. No. 2,2e-49;  
 Matches 132; Conservative 39; Mismatches 84; Indels 10; Gaps 4;

QY 2 YLSECKTGNGKNGYGTMSKTNGITCOKMSSTSPHPRPSPATHPSEGLEENYCRNPDND 61  
 DB 125 YIRNCLIGKGSYKGVISITKSIKQOPNMSMIPHHSFLPSSYRGKDIQENYCRNPRGE 184  
 QY 62 PGGPWCYTTDPKRYDYCDILECEB-ECMHGSGENYDGKISKTMSGLECOQANDSQSPHAA 120  
 DB 185 EGGPWCFTSNPEVRYEVCDFPQSEVCEMTCNGESYRGPMHDSKTCQRMDOQPRH 244  
 QY 121 GYIPSPKPNKLNKKYCNRPDRRLRPWCFTTDPKRWELCDIPRC-----TTPPSSGP 174

DB 245 KFLPERIPDGFPDNDYCRNPDGQGRPMVCYTLDPHTREYCAIKTCADNTMNDVPLETT 302  
 QY 175 QCLKGTGENYRGNAVAVTSQHTCOHWSAQTPHTERTPENPCKNLDENYCRNPDGR 234  
 DB 303 ECIQGGEGYRGVNTIWMGIPCORWDSQYPRHEDHTPENFKCKDLRENYCRNPDGAE 362  
 QY 235 WCHTNSQVWMEYC-KIPSCDSS 258  
 DB 363 WCFTTDPNIRVGYCSQIPKCDVS 387

## RESULT 10

151283  
 hepatocyte growth factor precursor - clawed frog  
 N/Alternate names: hepatoinetin A; scatter factor  
 C/Species: Xenopus sp. (clawed frog)  
 C/Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 09-May-2004  
 C/Accession: I51283  
 R/Nakamura, H.; Tashiro, K.; Nakamura, T.; Shiohara, K.  
 Mech. Dev. 49, 123-131, 1995  
 A/Title: Molecular cloning of Xenopus HGF cDNA and its expression studies in Xenopus ea  
 A/Reference number: I51283; MUID:95267690; PMID:7748783  
 A/Accession: I51283  
 A/Status: preliminary; translated from GB/EMBL/DBJ  
 A/Molecule type: mRNA  
 A/Residues: 1-710 <NAA>  
 A/Cross-references: GB:S77422; NID:9998932; PIDN:AA34354.1; PID:9998933  
 A/Note: the authors' translation for residue 458 (Thr) is inconsistent with the nucleot  
 C/Complex: disulfide-bonded heterodimer of chains derived from the same precursor  
 C/Function:  
 A/Description: stimulates mitosis of hepatocytes and other cells  
 A/Note: does not have proteinase activity  
 C/Superfamily: hepatocyte growth factor/macrocyte stimulating protein 1; kringe homolo  
 C/Keywords: duplication; glycoprotein; growth factor; heterodimer; kringe  
 F.42-477/478-709/Product: hepatocyte growth factor #status predicted <MAT>  
 F.42-477/Domain: hepatocyte growth factor alpha chain #status predicted <ACH>  
 F.115-193/Domain: kringe homology <KR1>  
 F.198-275/Domain: kringe homology <KR2>  
 F.289-367/Domain: kringe homology <KR3>  
 F.375-453/Domain: kringe homology <KR4>  
 F.478-709/Domain: hepatocyte growth factor beta chain #status predicted <BCH>  
 F.478-700/Domain: trypsin homology <TRY>  
 F.52/128/281/322/379/550/637/666/Binding site: carbohydrate (Asn) (covalent) #status pr  
 F.470-588/Disulfide bonds: #status predicted

Query Match 50.4%; Score 776.5; DB 1; Length 710;  
 Best Local Similarity 50.0%; Pred. No. 5.4e-49;  
 Matches 130; Conservative 39; Mismatches 88; Indels 3; Gaps 3;

QY 2 YLSECKTGNGKNGYGTMSKTNGITCOKMSSTSPHPRPSPATHPSEGLEENYCRNPDND 61  
 DB 111 YIRNCLIGKGSNNGYTRNVTGRGLACQPMNSMIPHHSFLPSTYRGKDLKKNYCRNPKGE 170  
 QY 62 PGGPWCYTTDPKRYDYCDILECEB-ECMHGSGENYDGKISKTMSGLECOQANDSQSPHAA 120  
 DB 171 EGGPWCFTSNPEVRYEVCDFPQSEVCEMTCNGESYRGPMHDSKTCQRMDOQPRH 230  
 QY 121 GYIPSPKPNKLNKKYCNRPDRRLRPWCFTTDPKRWELCDIPRC--TTPPSSGP 179  
 DB 231 KFLPERIPDGFPDNDYCRNPDGQGRPMVCYTLDPHTREYCAIKTCADNTMNDVPLETT 290  
 QY 180 KGTGENYRGNAVAVTSQHTCOHWSAQTPHTERTPENPCKNLDENYCRNPDGRAP 239  
 DB 291 KGGEGYRGVNTIWMGIPCORWDSQYPRHEDHTPENFKCKDLRENYCRNPDGSESP 350  
 QY 240 TTSQVWMEYC-KIPSCDSS 258  
 DB 351 TTDNIRIGHCSQIKKCOAS 370

## RESULT 11

A60185  
 hepatocyte growth factor precursor - mouse



N:Alternate names: hepatocytin A; scatter factor  
C:Species: Mus musculus (house mouse)  
C>Date: 03-Mar-1993 #sequence, revision 26-May-1994 #ext change 09-Jul-2004  
C:Accession: J02117; PC2064; A60185; S43416; S45521; S17173; S10966; I48758; J00231  
R:Sasaki, M.; Nishio, M.; Sasaki, T.; Enami, J.  
Biochem. Biophys. Res. Commun. 199, 772-779, 1994  
A:Title: Identification of mouse mammary fibroblast-derived mammary growth factor as hep  
A:Reference number: J02117; MUID:94183257; PMID:8135822  
A:Accession: J02117  
A:Molecule type: mRNA  
A:Residues: 1-728 <SAS2>  
A:Cross-references: UNIPROT:008048; GB:DI0212; NID:9220435; PIDN:BA01064.1; PID:9220436  
A:Experimental source: fibroblast, COS-1 cell  
A>Note: Submitted to JIPID, May 1993  
A:Accession: PC2064  
A:Molecule type: protein  
A:Residues: 496-504 <SA2>  
R:Rosen, E.M.; Meromsky, L.; Selter, E.; Winter, D.W.; Goldberg, I.D.  
Proc. Soc. Exp. Biol. Med. 195, 34-43, 1990  
A:Title: Purified scatter factor stimulates epithelial and vascular endothelial cell mig  
A:Reference number: A60185; MUID:90377927; PMID:2144630  
A:Accession: A60185  
A:Molecule type: protein  
A:Residues: 'X',184-188,'KX',191-192,'X',194,'XX',197,357-364,'XX',367,375-377,'E',379,'  
R:Lin, Y., Michalopoulos, G.K.; Zarnegar, R.  
Biochim. Biophys. Acta 1216, 299-303, 1993  
A:Title: Molecular cloning and characterization of cDNA encoding mouse hepatocyte growth  
A:Reference number: S43416; MUID:94060105; PMID:8241272  
A:Accession: S43416  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-728 <LIU>  
R:Lin, Y.  
A:Cross-references: EMBL:X72307  
A:Reference number: S45521  
A:Accession: S45521  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-563,'H',565-728 <LI2>  
A:Cross-references: EMBL:X72307  
R:Cofter, A.; Fellows, J.; Young, S.; Pappin, D.; Rahman, D.  
Biochem. J. 278, 35-41, 1991  
A:Title: Purification and characterization of biologically active scatter factor from ra  
A:Reference number: S17173; MUID:91354223; PMID:1831975  
A:Accession: S17173  
A:Molecule type: protein  
A:Residues: 496-517,'R',519 <COR>  
R:Gherardi, E.; Stoker, M.  
Nature 346, 228, 1990  
A:Title: Hepatocytes and scatter factor.  
A:Reference number: S10966; MUID:90326152; PMID:2142751  
A:Accession: S10966  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 456-507,'X',509-512,'L',514-516,'X',518-519 <NAT>  
R:Plaschke-Schluter, A.; Behrens, J.; Gherardi, E.; Birchmeier, W.  
J. Biol. Chem. 270, 830-836, 1995  
A:Title: Characterization of the scatter factor/hepatocyte growth factor gene promoter.  
A:Reference number: I48758; MUID:95125332; PMID:7822318  
A:Accession: I48758  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-30 <RES>  
A:Cross-references: EMBL:X81630; NID:9673451; PIDN:CA57206.1; PID:9673452  
C:Function: disulfide-bonded heterodimer of chains derived from the same precursor  
A:Description: stimulates mitosis of hepatocytes and other cells  
A>Note: does not have proteinase activity  
C:Superfamily: hepatocyte growth factor/macrophage stimulating protein 1; kringle homol  
C:Keywords: alternative splicing; glycoprotein; growth factor; heterodimer; kringle; pyr  
F:156-495,496-728/Product: hepatocyte growth factor #status predicted <MAT>

F:56-495/Domain: hepatocyte growth factor alpha chain #status predicted <ACH>  
F:129-207/Domain: kringle homology <KR1>  
F:212-289/Domain: kringle homology <KR2>  
F:306-384/Domain: kringle homology <KR3>  
F:392-470/Domain: kringle homology <KR4>  
F:496-728/Domain: hepatocyte growth factor beta chain #status predicted <BCH>  
F:496-719/Domain: trypsin homology <TRY>  
F:33/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predi  
F:295,403,569,656/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F:488-607/Disulfide bonds: #status predicted

Query Match 50.4%; Score 776; DB 1; Length 728;  
Best Local Similarity 49.4%; Pred. No. 66-49;  
Matches 131; Conservative 40; Mismatches 84; Indels 10; Gaps 4;

Qy 2 YLSECKTGKNGKRYGKMTSKKNGITCOAKSSSTSPHPPSPATHPSEGLBENYCRPNDD 61  
Db 125 YINCCIIGKSGSYKGVSTIKSGIKCOPNMSMIPHHSFLPSYSRKADQENYCRPNRGE 184  
Qy 62 POGPWCYTTDPKRYDYCDILECEE-ECMHSGENYDGKISKTMGLCOAMPDSQSPHAF 120  
Db 185 EGPPWCFTSNPEVRYEVCIDPQCSVEECMTNGESTYRGPDHTESKTCORWDQTPHRH 244  
Qy 121 GYIPSKFPNKLKKNYCRNPDELAPWCFTTDPNKRWECDIPRCT-----TPPSSGP 174  
Db 245 KFLPERYPDKGPDNCRNDGKRPWCCTLDPTDTEWCAIKTCAHSVNETDVME-- 302  
Qy 175 TYOCLKGTGNTGNVAIVYSGTCQWMSAQTPHTERPENPCNLDENYCRNPDGKR 234  
Db 303 TTECIQGGEGYGTSTNTIWNIGIPCORWDSQYPHKHIDITPENKCKDLRENNYCRNPDGAE 362  
Qy 235 APWCHTTNSQVRWEYC-KIPSCDS 258  
Db 363 SPWCFTTDPNIRKVGCSQIPKCDVS 387

RESULT 12  
J05061  
C:Species: Rattus norvegicus (Norway rat)  
C>Date: 31-Jan-1997 #sequence, revision 31-Jan-1997 #ext change 09-Jul-2004  
C:Accession: J05061  
R:Ohshiro, K.; Iwama, A.; Matsuno, K.; Ezaki, T.; Sakamoto, O.; Hamaguchi, I.; Takaue,  
Biochem. Biophys. Res. Commun. 227, 273-280, 1996  
A:Title: Molecular cloning of rat macrophage-stimulating protein and its involvement in  
A:Reference number: J05061; MUID:97011126; PMID:8858136  
A:Accession: J05061  
A:Molecule type: mRNA  
A:Residues: 1-716 <OHS>  
A:Cross-references: UNIPROT:P70521; EMBL:X95096; NID:91669718; PIDN:CA64473.1; PID:916  
C:Superfamily: hepatocyte growth factor/macrophage stimulating protein 1; kringle homol  
C:Keywords: duplication; glycoprotein; growth factor; kringle  
F:1-31/Domain: signal sequence #status predicted <SIG>  
F:32-488/Domain: macrophage-stimulating protein 1 #status predicted <MAT>  
F:32-488/Domain: macrophage-stimulating protein 1 alpha chain #status predicted <ACH>  
F:191-268/Domain: kringle homology <KR1>  
F:292-370/Domain: kringle homology <KR2>  
F:379-457/Domain: kringle homology <KR3>  
F:489-716/Domain: macrophage-stimulating protein 1 beta chain #status predicted <BCH>  
F:489-709/Domain: trypsin homology <TRY>  
F:72,305,620/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 49.8%; Score 766.5; DB 1; Length 716;  
Best Local Similarity 48.5%; Pred. No. 2,96-48;  
Matches 132; Conservative 36; Mismatches 89; Indels 15; Gaps 5;

Qy 2 YLSECKTGKNGKRYGKMTSKKNGITCOAKSSSTSPHPPSPATHPSEGLBENYCRPNDD 61  
Db 106 YVRTIMDGAISYRGTVAATADGLPCQWMSRRFPNDHKTPTP--PKNGLEENPCRNPD 163  
Qy 62 POGPWCYTTDPKRYDYCDILECEE-CMHSGENYDGKISKTMGLCOAMPDSQSPHAF 120

Db 164 PRGPMCTTNRSVFQSCGKISCREAVCWGCEVDYRGEDVYESGECQRMQLQHPHSH 223  
Qy 121 GYISKEPNKLNKQYCRNDRRLRPWCFTTDPNKRELCDIPRC--TPPPSSGPTQ- 177  
Db 224 PPHKFPDQALNDKNCRNPDASERPMWCYTTDPNVEREFCDLPSGPNLPPTTKSGSKSQ 283  
Qy 178 -----CLKGTGENYRGNVAVTSGHTCOHWSAOTPHHTHPENPCKNLDENYCN 229  
Db 284 RNKVAKNCRRGEGEDYRGTTNTTSAGVPCQRMDAQPHQHRFVPEKAYCKDLRENFCRN 343  
Qy 230 PDGKAPWCHTTNSQVRYEYC-KIPSCDSSPV 260  
Db 344 PDGSEAPWCTTSRGRVAFVCYIPRCTEEV 375  
RESULT 13  
151285  
~hepatocyte growth factor/scatter factor - chicken (fragment)  
C/Species: Gallus gallus (chicken)  
C/Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #ext\_change 09-Jul-2004  
C/Accession: F51285  
R/Streit, A.; Stern, C.D.; Thery, C.; Ireland, G.W.; Aparicio, S.; Sharpe, M.J.; Gerard  
Development 121, 813-824, 1995  
A/Title: A role for HGF/SF in neural induction and its expression in Hensen's node durin  
A/Reference number: F51285; PMID:95237013; PMID:7720585  
A/Accession: F51285  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: mRNA  
A/Residues: 1-411 <STR>  
C/Superfamily: hepatocyte growth factor/macrophage stimulating protein 1; kringe homolo  
F:124-197/Domain: kringe homology <KR3>  
F:202-279/Domain: kringe homology <KR2>  
F:296-374/Domain: kringe homology <KR3>  
Query Match 49.0%; Score 754.5; DB 2; Length 411;  
Best Local Similarity 50.2%; Pred. No. 1.2e-47;  
Matches: 132; Conservative 31; Mismatches 89; Indels 11; Gaps 4;  
Qy 2 YLSECKTNGKNGYRGTMSKTNGITCOKWSSTSPHRPRSPATHPSEGLEENYCRNDND 61  
Db 120 YVRNCIIGKALYKGIITKSGIOQANSMIPHE-----HSYKQKLRNYCNRNPG 174  
Qy 62 PGGWCYTTDPKRYDYCDILECEE-ECMHCSEYNDGKISKTMSGLECOAMDQSPPAH 120  
Db 175 EGGPWCFTTSPQMRHVCIDIPLCSEVECWTCNGESYRGMHTSGECQRMWDLQRPKH 234  
Qy 121 GYISKEPNKLNKQYCRNDRRLRPWCFTTDPNKRELCDIPRC--TPPPSS- -GPT 176  
Db 235 KFRPRYVDPKGFDDYCRNPDGLRPWCYTTDPNTPWECALKTCDVGLNSTEVAEET 294  
Qy 177 CLKGTGENYRGNVAVTSGHTCOHWSAOTPHHTHPENPCKNLDENYCNPDGRAP 236  
Db 225 TCIQOGSEYRKTAVTNTSGIOQKNDSPQHONHTPBNFKCKDLRENYCNDPDSSE 354  
Qy 237 WCHTNSQVRYEYC-KIPSCDSS 258  
Db 355 WCFTDPNIRIGYCSQIPKCVS 377  
RESULT 14  
A0332  
macrophage-stimulating protein 1 precursor - mouse  
N/Alternate names: hepatocyte growth factor-like protein  
C/Species: Mus musculus (house mouse)  
C/Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #ext\_change 09-Jul-2004  
C/Accession: A0332; B40332  
R/Degen, S.J.F.; Stuart, L.A.; Han, S.; Jamison, C.S.  
Biochemistry 30, 9781-9791, 1991  
A/Title: Characterization of the mouse cDNA and gene coding for a hepatocyte growth fac  
A/Reference number: A0332; PMID:92002017; PMID:1832957  
A/Accession: A0332

A/Molecule type: DNA  
A/Residues: 1-716 <DEG>  
A/Cross-references: UNIPROT:P26928; GB:M74180; NID:G193831; PID:AAA50166.1; PID:G19383;  
A/Accession: B40332  
A/Molecule type: mRNA  
A/Residues: 1-18 'P' 20-716 <DEG2>  
A/Cross-references: GB:M74181; NID:G193833; PID:AAA50167.1; PID:G193834  
C/Genetics:  
A/Intons: 18/1; 67/2; 105/1; 143/2; 189/1; 229/2; 269/1; 334/2; 378/1; 412/2; 458/1; 4  
C/Complex: disulfide-bonded heterodimer of chains derived from the same precursor  
C/Superfamily: hepatocyte growth factor/macrophage stimulating protein 1; kringe homolo  
C/Keywords: duplication; glycoprotein; growth factor; kringe  
F:1-31/Domain: signal sequence #status predicted <SIG>  
F:19-488/489-716/Product: macrophage-stimulating protein 1 #status experimental <MAT>  
F:110-186/Domain: alpha chain #status experimental <ACH>  
F:191-268/Domain: kringe homology <KR1>  
F:292-370/Domain: kringe homology <KR2>  
F:379-457/Domain: kringe homology <KR3>  
F:484-711/Domain: beta chain #status experimental <BCH>  
F:489-709/Domain: trypsin homology <TRY>  
F:72,173,305,620/Binding site: carbohydrate (Asn) (covalent) #status predicted  
Query Match 48.9%; Score 753.5; DB 1; Length 716;  
Best Local Similarity 48.3%; Pred. No. 2.5e-47;  
Matches: 129; Conservative 37; Mismatches 86; Indels 15; Gaps 5;  
Qy 2 YLSECKTNGKNGYRGTMSKTNGITCOKWSSTSPHRPRSPATHPSEGLEENYCRNDND 61  
Db 106 YVRCINDNGSVYGTARTAGLPCQAMSRFPNDKRTPT--PKNGLEENFCRNDGCD 163  
Qy 62 PGGWCYTTDPKRYDYCDILECEE-ECMHCSEYNDGKISKTMSGLECOAMDQSPPAH 120  
Db 164 PRGPMCTTNRSVFQSCGKISCREAVCWGCEVDYRGEDVYESGECQRMQLQHPHSH 223  
Qy 121 GYISKEPNKLNKQYCRNDRRLRPWCFTTDPNKRELCDIPRC--TPPP----- 170  
Db 224 PPHKFPDQALNDKNCRNPDASERPMWCYTTDPNVEREFCDLPSGPNLPPTTKSGSKSQ 283  
Qy 171 -SSGPTVCLKGTGENYRGNVAVTSGHTCOHWSAOTPHHTHPENPCKNLDENYCN 229  
Db 284 RNKVAKNCRRGEGEDYRGTTNTTSAGVPCQRMDAQPHQHRFVPEKAYCKDLRENFCRN 343  
Qy 230 PDGKAPWCHTTNSQVRYEYC-KIPSC 255  
Db 344 PDGSEAPWCTTSRGRVAFVCYIPRCTEEV 370  
RESULT 15  
S00657  
apoprotein(a) (EC 3.4.21.-) precursor [validated] - human  
N/Alternate names: apolipoprotein(a); lipoprotein(a) chain apo(a)  
C/Species: Homo sapiens (man)  
C/Date: 30-Jun-1989 #sequence\_revision 30-Jun-1989 #ext\_change 09-Jul-2004  
C/Accession: S00657; A28017; B47277; I60906; A47233; I52415; I65286  
R/Mclean, J.W.; Tomlinson, J.B.; Kuang, W.T.; Baton, D.L.; Fless, G.M.; Scar  
Nature 330, 132-137, 1987  
A/Title: cDNA sequence of human apolipoprotein(a) is homologous to plasminogen.  
A/Reference number: S00657; PMID:88039109; PMID:3670400  
A/Accession: S00657  
A/Molecule type: mRNA  
A/Residues: 1-4548 <MCL>  
A/Cross-references: UNIPROT:P08519; GB:X06290; EMBL:X06696; NID:G28619; PID:CAA29618.1;  
R/Baton, D.L.; Fless, G.M.; Kohr, W.T.; McLean, J.W.; Xu, Q.T.; Miller, C.G.; Lawn, R.M.  
Proc. Natl. Acad. Sci. U.S.A. 84, 3224-3228, 1987  
A/Title: Partial amino acid sequence of apolipoprotein(a) shows that it is homologous to  
A/Reference number: A28017; PMID:87204109; PMID:3472206  
A/Accession: A28017  
A/Molecule type: protein  
A/Residues: 20-21 'P' 23-34; 177-179, 'N', 181-186, 'T', 188-196, 'DKG', 200, 292-314, 'W', 316-31  
X', 4396-4401 <EM>  
R/Wade, D.P.; Clarke, J.G.; Lindahl, G.E.; Liu, A.C.; Zybow, B.R.; Meier, K.; Schwartz, K  
Proc. Natl. Acad. Sci. U.S.A. 90, 1369-1373, 1993

A>Title: 5' control regions of the apolipoprotein(a) gene and members of the related pla  
 A.Reference number: A47277; MUID:93165698; PMID:7679504  
 A.Accession: A47277  
 A>Status: preliminary; translation not shown; translated from GB/EMBL/DBJ  
 A.Molecule type: DNA  
 A.Residues: 1-16 <RES>  
 A.Cross-references: GB:J07899; NID:9967973; PID:9967974  
 R.Margaret, N.; Acquati, F.; Magnaghi, P.; Bruno, L.; Pontoglio, M.; Rocchi, M.; Sacco  
 Proc. Natl. Acad. Sci. U.S.A. 89, 11584-11588, 1992  
 A>Title: Characterization by yeast artificial chromosome cloning of the linked apolipop  
 A.Reference number: A47233; MUID:93087573; PMID:1454851  
 A.Accession: 160906  
 A>Status: preliminary; translated from GB/EMBL/DBJ  
 A.Molecule type: DNA  
 A.Residues: 1-16 <RES>  
 A.Cross-references: GB:M90078; NID:9178786; PID:AAA5547.1; PID:9553188  
 A.Note: apo(a) gene 1 (nomenclature of reference 152415)  
 A.Accession: A47233  
 A>Status: preliminary; translation not shown; translated from GB/EMBL/DBJ  
 A.Molecule type: DNA  
 A.Residues: 1-16 <RES>  
 A.Cross-references: GB:M90079; NID:9178784; PID:AAA5546.1; PID:9553187  
 R.Ichiyose, A.  
 Biochemistry 31, 3113-3118, 1992  
 A>Title: Multiple members of the plasminogen-apolipoprotein(a) gene family associated w  
 A.Reference number: 152415; MUID:92207924; PMID:1554698  
 A.Accession: 152415  
 A>Status: preliminary; translated from GB/EMBL/DBJ  
 A.Molecule type: DNA  
 A.Residues: 1-16 <RES>  
 A.Cross-references: GB:M86877; NID:9178780; PID:AAA49909.1; PID:9553185  
 A.Note: apo(a) gene 1 (nomenclature of reference 152415)  
 A.Accession: 152415  
 A>Status: preliminary; translated from GB/EMBL/DBJ  
 A.Molecule type: DNA  
 A.Residues: 1-16 <RES>  
 A.Cross-references: GB:M86878; NID:9178782; PID:AAA51749.1; PID:9553186  
 C.Genetics:  
 A.Gene: GDB:LPA  
 A.Cross-references: GDB:120699; OMIM:152200  
 A.Map position: 6q26-6q27  
 A.Note: several genes closely linked on chromosome 6 are identical in the first coding e  
 ts of kringle repeats  
 C/Superfamily: apolipoprotein(a); kringle homology; trypsin homology  
 C/Keywords: hydrolase; kringle; lipid binding; lipoprotein; serine proteinase  
 F:1-19/Domain: signal sequence #status predicted <SIG>  
 F:20-4548/Product: apolipoprotein(a) #status experimental <Mat>  
 F:28-105/Domain: kringle homology <KR1>  
 F:142-219/Domain: kringle homology <KR2>  
 F:256-333/Domain: kringle homology <KR3>  
 F:370-447/Domain: kringle homology <KR4>  
 F:484-561/Domain: kringle homology <KR5>  
 F:598-675/Domain: kringle homology <KR6>  
 F:712-789/Domain: kringle homology <KR7>  
 F:826-903/Domain: kringle homology <KR8>  
 F:940-1017/Domain: kringle homology <KR9>  
 F:1054-1131/Domain: kringle homology <KR10>  
 F:1168-1245/Domain: kringle homology <KR11>  
 F:1282-1359/Domain: kringle homology <KR12>  
 F:1396-1473/Domain: kringle homology <KR13>  
 F:1510-1587/Domain: kringle homology <KR14>  
 F:1624-1701/Domain: kringle homology <KR15>  
 F:1738-1815/Domain: kringle homology <KR16>  
 F:1852-1929/Domain: kringle homology <KR17>  
 F:1966-2043/Domain: kringle homology <KR18>  
 F:2080-2157/Domain: kringle homology <KR19>  
 F:2194-2271/Domain: kringle homology <KR20>  
 F:2308-2385/Domain: kringle homology <KR21>  
 F:2422-2499/Domain: kringle homology <KR22>  
 F:2536-2613/Domain: kringle homology <KR23>  
 F:2650-2727/Domain: kringle homology <KR24>  
 F:2764-2841/Domain: kringle homology <KR25>  
 F:2878-2955/Domain: kringle homology <KR26>

F:2992-3069/Domain: kringle homology <KR27>  
 F:3106-3183/Domain: kringle homology <KR28>  
 F:3220-3297/Domain: kringle homology <KR29>  
 F:3334-3411/Domain: kringle homology <KR30>  
 F:3448-3525/Domain: kringle homology <KR31>  
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 F:3676-3753/Domain: kringle homology <KR33>  
 F:3782-3859/Domain: kringle homology <KR34>  
 F:3896-3973/Domain: kringle homology <KR35>  
 F:4010-4087/Domain: kringle homology <KR36>  
 F:4124-4201/Domain: kringle homology <KR37>  
 F:4228-4307/Domain: kringle homology <KR38>  
 F:4328-4541/Domain: trypsin homology <TRY>

Query Match 48.64; Score 749; DB 1; Length 4548;  
 Best Local Similarity 41.24; Pred. No. 3.3e-46;  
 Matches 129; Conservative 45; Mismatches 81; Indels 58; Gaps 5;

Qy 3 LSECKTNGKNGVYRGVTSKTKNGITTCQKWSSTSPHRRPSPATPSGLENYCRNDNDP 62  
 Db 3779 VQDCYHGDGQSYRGSPSTVTGRTQSWSMTPHMHQRTTEYYPNGGLTRNYCRNDPAE1 3838  
 Qy 63 QGFWCTTTPPEKRYDYCDILECE-----ECM 89  
 Db 3839 R-FWCTTMDPSVWMEYCNLTQCVMESTLLTPTVVPVSTELPSEAPTESTGVQDCY 3897  
 Qy 90 HSGENVYDGKISKTMGLBEOAMDSSPHAHGYIPKPPKXNKKNYCRNDRELAPWCF 149  
 Db 3898 RGDGQSTRGTLSTTIGRTQSWSMTPHMHRIPLYPPAGLTRYNCRNDPEIRWCY 3957  
 Qy 150 TTPDNKRWELCDIPRC-----TTP-----PSSGPTYQ-CLAKGTEN 185  
 Db 3958 TMDPSVWMEYCNLTQCPYESSVLTPPYAPVSTELAPSEQAPPEKSPVQDCYHGDGRS 4017  
 Qy 186 YRGNAVTVSGTQKWSAQTPHTERTPBNPCNLDENYCRNDPKRAIPWCHTNSQV 245  
 Db 4018 YRGISSTVYVGRYQSWSMIPMHQRTPEYNPAGLTENYCRNDPSGKQPCYCTDPCV 4077  
 Qy 246 RMEYCKIPSCDS 258  
 Db 4078 RMEYCNLTQCSST 4090

Search completed: July 27, 2005, 03:30:30  
 Job time: 17 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 27, 2005, 03:21:14 ; Search time 61 Seconds

(without alignments)  
2182.633 Million cell updates/sec

Title: US-09-502-176-2

Perfect score: 1540

Sequence: 1 VYLSECKTGNGKRYRGTMK.....TNSQVAMEYCKIPSCDSSPV 260

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: UniProt\_03:\*

1: uniprot\_sprot:\*

2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1535	99.7	810	1	PLNM_HUMAN
2	1442	93.6	810	1	PLNM_MACMU
3	1306	84.8	359	2	08WMRI
4	1299	84.4	812	1	PLNM_RAT
5	1292	83.9	790	1	PLNM_PIG
6	1291	83.8	812	1	PLNM_BOVIN
7	1279	83.1	466	2	06TCIO
8	1279	83.1	812	1	PLNM_MOUSE
9	1237	80.3	810	1	PLNM_ERIEU
10	1203.5	78.1	759	2	07TP84
11	1160	75.3	806	1	PLNM_MACMU
12	996	64.7	818	2	06PBA6
13	881	57.2	2869	2	028398
14	809.5	52.6	449	2	06GP14
15	809.5	52.6	716	2	091691
16	797	51.8	728	1	HGF_HUMAN
17	796	51.7	709	2	07ZTN9
18	795.5	51.7	717	2	P70006
19	782	50.8	728	1	HGF_RAT
20	778	50.5	726	2	090978
21	778	50.5	730	2	086787
22	777	50.5	728	2	086787
23	776.5	50.4	710	2	086787
24	776	50.4	728	1	HGF_MOUSE
25	774	50.3	730	2	076ES1
26	772	50.1	704	2	090865
27	772	50.1	728	2	090865
28	766.5	49.8	709	2	0902N6
29	766.5	49.8	716	2	P70521
30	754.5	49.0	405	2	0788Q2
31	753.5	48.9	716	1	HGFL_MOUSE

32	753.5	48.9	716	2	091XG8	091XG8 mus musculus
33	749	48.6	4548	1	AP0A_HUMAN	P08519 homo sapien
34	739	48.0	711	1	HGFL_HUMAN	P26927 homo sapien
35	739	48.0	1420	1	AP0A_MACMU	P14417 macaca mula
36	709	46.0	567	2	013208	013208 homo sapien
37	643	41.8	648	2	09H1V4	09H1V4 homo sapien
38	503	32.7	454	2	046506	046506 papio hamad
39	459.5	29.8	215	2	042341	042341 gallus gall
40	458.5	29.8	429	2	08AVB0	08AVB0 brachydanto
41	412.5	26.8	615	2	06GNK4	06GNK4 xenopus lae
42	407.5	26.5	607	2	06DPF5	06DPF5 xenopus lae
43	400	26.0	209	2	08BS17	08BS17 mus musculus
44	391.5	25.4	325	1	PLNM_PETMA	P33574 petromyzon
45	383	24.9	948	2	09Y1Y6	09Y1Y6 ephedalia f

## ALIGNMENTS

RESULT 1

ID	PLNM_HUMAN	STANDARD	PRT	810 AA.
AC	P00747; OL5146; O6PA00;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	01-MAR-1989 (Rel. 10, Last sequence update)			
DT	25-OCT-2004 (Rel. 45, Last annotation update)			
DE	Plasminogen precursor (EC 3.4.21.7) [Contains: Angiostatin].			
GN	Name:PLG;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RX	SEQUENCE FROM N.A., AND VARIANT ASN-472.			
RA	MEDLINE=90202879; PubMed=2318848;			
RT	Petersen T.E., Martzen M.R., Ichinose A., Davie E.W.;			
RT	"Characterization of the gene for human plasminogen, a key proenzyme			
RT	in the fibrinolytic system.";			
RT	J. Biol. Chem. 265:6104-6111(1990).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=87162490; PubMed=3030813; DOI=10.1016/0014-5793(87)81501-6;			
RA	Forrester M., Raden B., Israelsson M., Larsson K., Heden L.-O.;			
RT	"Molecular cloning and characterization of a full-length cDNA clone			
RT	for human plasminogen.";			
RT	FEBS Lett. 213:254-260(1987).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Liver;			
RA	Browne M.J., Chapman C.G., Dodd I., Carey J.E., Lawrence G.M.P.,			
RA	Mitchell D., Robinson J.H.;			
RT	"Expression of recombinant human plasminogen and aglycoplasminogen in			
RT	HeLa cells.";			
RT	Submitted (OCT-1991) to the EMBL/GenBank/DBJ databases.			
RN	[4]			
RP	SEQUENCE FROM N.A., AND VARIANTS LYS-57; GLN-133; HIS-261; TRP-408;			
RP	ASN-472; VAL-494 AND TRP-523.			
RA	Rieder M.J., Arnel T.Z., Carrington D.P., Ozuna M., Kulaneck S.A.,			
RA	Rajkumar N., Torch E.J., Yi Q., Nickerson D.A.;			
RT	"Sequences, NDBI HL66682 program for genomic applications, UW-			
RT	PHRC, Seattle, WA (URL: http://pga.gs.washington.edu).";			
RT	Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.			
RN	[5]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Kidney;			
RX	MEDLINE=23386257; PubMed=12477932; DOI=10.1073/pnas.242603899;			
RA	Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,			
RA	Klauser R.D., Collins F.S., Wagner L., Shermen C.M., Schuler G.D.,			
RA	Altschul S.F., Zeeberg B., Buelow K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,			
RA	Ditachenko L., Marsina K., Farmer A.A., Rubin G.M., Hong L.,			
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,			
RA	Brownstein M.J., Udell T.B., Toshitaki S., Carninci P., Prange C.,			

- RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S.C., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butcherfield Y.S.N., Krzywicki M.J., Skalska U., Smalhus D.B.,  
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [6]  
 RP SEQUENCE OF 20-810, AND VARIANT ASN-472.  
 RA Sottrup-Jensen L., Petersen T.E., Magnusson S.;  
 RL Submitted (JUL-1977) to the PIR data bank.  
 RN [7]  
 RP SEQUENCE OF 292-810 FROM N.A.  
 RA MEDLINE=8502311; PubMed=6148961;  
 RA Malinowski D.P., Sadler J.E., Davie E.W.;  
 RT "Characterization of a complementary deoxyribonucleic acid coding for  
 RT human and bovine plasminogen.";  
 RL Biochemistry 23:4243-4250(1984).  
 RN [8]  
 RP SEQUENCE OF 20-100.  
 RA MEDLINE=75093329; PubMed=122932;  
 RA Wiman B., Wallen P.;  
 RT "Structural relationship between 'glutamic acid' and 'lysine' forms of  
 RT human plasminogen and their interaction with the NH2-terminal  
 RT activation peptide as studied by affinity chromatography.";  
 RL Eur. J. Biochem. 50:489-494(1975).  
 RN [9]  
 RP SEQUENCE OF 95-380; 581-626; 657-700 AND 732-810, AND VARIANT ASN-472.  
 RA Sottrup-Jensen L., Claess H., Zaidel M., Petersen T.E., Magnusson S.;  
 RA (in) Davidson J.F., Royan R.M., Samama M.M., Desnoyers P.C. (eds.);  
 RL Progress in Chemical Fibrinolysis and Thrombolysis, pp.3:191-209,  
 RL Raven Press, New York (1978).  
 RN [10]  
 RP SEQUENCE OF 483-604.  
 RA MEDLINE=76043692; PubMed=126863;  
 RA Wiman B., Wallen P.;  
 RT "Amino-acid sequence of the cyanogen-bromide fragment from human  
 RT plasminogen that forms the linkage between the plasmin chains.";  
 RL Eur. J. Biochem. 58:539-547(1975).  
 RN [11]  
 RP SEQUENCE OF 581-810.  
 RA MEDLINE=77225245; PubMed=142009;  
 RA Wiman B.;  
 RT "Primary structure of the B-chain of human plasmin.";  
 RL Eur. J. Biochem. 76:129-137(1977).  
 RN [12]  
 RP ACTIVE SITE.  
 RA MEDLINE=73149248; PubMed=4694729;  
 RA Robbins K.C., Bernabe P., Arzadon L., Summaria L.;  
 RT "The primary structure of human plasminogen. II. The histidine loop of  
 RT human plasmin: 1191 (B) chain active center histidine sequence.";  
 RL J. Biol. Chem. 248:1631-1633(1973).  
 RN [13]  
 RP ACTIVE SITE.  
 RA MEDLINE=69234739; PubMed=4240117;  
 RA Groskopf W.R., Summaria L., Robbins K.C.;  
 RT "Studies on the active center of human plasmin. Partial amino acid  
 RT sequence of a peptide containing the active center serine residue.";  
 RL J. Biol. Chem. 244:3590-3597(1969).  
 RN [14]  
 RP OMEGA-AMINOCARBOXYLIC ACID-BINDING SITES.  
 RA MEDLINE=82213905; PubMed=6919539;  
 RA Trexler M., Vail Z., Patchy L.;  
 RT "Structure of the omega-aminocarboxylic acid-binding sites of human  
 RT plasminogen. Arginine 70 and aspartic acid 56 are essential for  
 RT binding of ligand by kringle 4.";  
 RL J. Biol. Chem. 257:7401-7406(1982).
- RN [15]  
 RP FIBRIN AND OMEGA-AMINOCARBOXYLIC ACID BINDING SITES.  
 RX MEDLINE=85054794; PubMed=6094326;  
 RA Vail Z., Patchy L.;  
 RT "The fibrin-binding site of human plasminogen. Arginines 32 and 34 are  
 RT essential for fibrin affinity of the kringle 1 domain.";  
 RL J. Biol. Chem. 259:13690-13694(1984).  
 RN [16]  
 RP PHOSPHORYLATION SITE SER-597.  
 RA MEDLINE=97345939; PubMed=9201956; DOI=10.1021/bj970328d;  
 RA Wang H., Piorok M., Bretthauer R.K., Castellino F.J.;  
 RT "Serine-578 is a major phosphorylation locus in human plasma  
 RT plasminogen.";  
 RL Biochemistry 36:8100-8106(1997).  
 RN [17]  
 RP CARBOHYDRATE-LINKAGE SITES.  
 RX MEDLINE=88185329; PubMed=3356193;  
 RA Marti T., Schaller J., Rickli E.E., Schmid K., Kamerling J.P.,  
 RA Gerwig G.J., van Halbeek H., Vliegenhart J.F.;  
 RT "The N- and O-linked carbohydrate chains of human, bovine and porcine  
 RT plasminogen. Species specificity in relation to stialylation and  
 RT fucosylation patterns.";  
 RL Eur. J. Biochem. 173:57-63(1988).  
 RN [18]  
 RP CARBOHYDRATE-LINKAGE SITE SER-268.  
 RX MEDLINE=97207306; PubMed=9054441; DOI=10.1074/jbc.272.11.7408;  
 RA Pirte-Shepherd S.R., Stevens R.D., Andon N.L., Enghild J.J.,  
 RA Pizzo S.V.;  
 RT "Evidence for a novel O-linked stialylated trisaccharide on Ser-248 of  
 RT human plasminogen 2.";  
 RL J. Biol. Chem. 272:7408-7411(1997).  
 RN [19]  
 RP CHARACTERIZATION OF ANGIOSTATIN, AND PARTIAL SEQUENCE.  
 RX MEDLINE=95042728; PubMed=7525077; DOI=10.1016/0092-8674(94)90200-3;  
 RA O'Reilly M.S., Holmgren L., Shing Y., Chen C., Rosenthal R.A.,  
 RA Moses M., Lane W.S., Cao Y., Sage E.H., Folkman J.;  
 RT "Angiostatin: a novel angiogenesis inhibitor that mediates the  
 RT suppression of metastases by a Lewis lung carcinoma.";  
 RL Cell 79:315-328(1994).  
 RN [20]  
 RP CHARACTERIZATION OF ANGIOSTATIN.  
 RX MEDLINE=97238710; PubMed=9102221;  
 RA Sim B.K., O'Reilly M.S., Liang H., Fortier A.H., He W., Maden J.W.,  
 RA Lapcevich R., Nacy C.A.;  
 RT "A recombinant human angiostatin protein inhibits experimental primary  
 RT and metastatic cancer.";  
 RL Cancer Res. 57:1329-1334(1997).  
 RN [21]  
 RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 374-461.  
 RX MEDLINE=92031502; PubMed=1657148;  
 RA Mlichnak A.M., Tulinsky A., Ravichandran K.G.;  
 RT "Crystal and molecular structure of human plasminogen kringle 4  
 RT refined at 1.9-A resolution.";  
 RL Biochemistry 30:10576-10586(1991).  
 RN [22]  
 RP X-RAY CRYSTALLOGRAPHY (2.25 ANGSTROMS) OF 374-461.  
 RX MEDLINE=92031503; PubMed=1657149;  
 RA Wu T.-P., Padmanabhan K., Tulinsky A., Mlichnak A.M.;  
 RT "The refined structure of the epsilon-aminocaproic acid complex of  
 RT human plasminogen kringle 4.";  
 RL Biochemistry 30:10589-10594(1991).  
 RN [23]  
 RP X-RAY CRYSTALLOGRAPHY (1.67 ANGSTROMS) OF 376-454.  
 RX MEDLINE=15299951;  
 RA Stec B., Yamano A., Whitlow M., Teeter M.M.;  
 RT "Structure of human plasminogen kringle 4 at 1.68 Angstrom and 277 K.  
 RT A possible structural role of disordered residues.";  
 RL Acta Crystallogr. D 53:169-178(1997).  
 RN [24]  
 RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 102-181.  
 RX MEDLINE=96180681; PubMed=8611560; DOI=10.1021/bi952135i;  
 RA Mathews I.I., Vanderhoff-Hanover P., Castellino F.J., Tulinsky A.;  
 RT "Crystal structures of the recombinant kringle 1 domain of human

RT plasminogen in complexes with the ligands epsilon-aminocaproic acid  
RT and trans-4-(aminomethyl) cyclohexane-1-carboxylic Acid.",

Query Match	99.7%	Score 1535;	DB 1;	Length 810;
Best Local Similarity	99.6%	Pred. No. 1.1e-108;		
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Db	98	YLSSEKTKNGKNYRGTMSTKNGITCOKKSSSTS	PHRPRSPATHSEGLEENYCRPN	157
QY	61	DPQPMCYTTDPKRYDYCDILICEEBCHMCSGENTDGI	SKTMSGLECAMDSOSP	120
Db	158	DPQPMCYTTDPKRYDYCDILICEEBCHMCSGENTDGI	SKTMSGLECAMDSOSP	217
QY	121	GYIPSKFPKKNLKONYCRNPDRRLRPMCFPTDNRKWE	LCDIRCTTPPPSSGPTQCL	180
Db	218	GYIPSKFPKKNLKONYCRNPDRRLRPMCFPTDNRKWE	LCDIRCTTPPPSSGPTQCL	277
QY	181	GTGENYRGNVAATVSGTCHQHSQAQTPHTHERTPEN	PPCKNLNDENTCRNPDGGRAPWCHT	240
Db	278	GTGENYRGNVAATVSGTCHQHSQAQTPHTHERTPEN	PPCKNLNDENTCRNPDGGRAPWCHT	357
QY	241	TNSOVRMEYCKIPSCDSSPV	260	
Db	338	TNSOVRMEYCKIPSCDSSPV	357	

	RESULT 2
CC	PLNM_MACMU
CC	ID PLNM_MACMU STANDARD; PRT; 810 AA.
AC	P12545;
DT	01-OCT-1989 (Rel. 12, Created)
DT	01-OCT-1989 (Rel. 12, Last sequence update)
DT	25-OCT-2004 (Rel. 45, Last annotation update)
DE	Plasminogen precursor (EC 3.4.21.7).
GN	Name=PLG;
OS	Macaca mulatta (Rheus macaque).
OC	Eukaryota; Metazoa; Chordata; Craniota; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Cereprothecidae;
OC	Cercopithecinae; Macaca.
OX	NCBI_TaxID=9544;
RN	[1]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=69174660; Pubmed=2925643;
RY	Tomlinson J.E., McLean J.W., Lawn R.M.;
RT	"Rhesus monkey apolipoprotein(a). Sequence, evolution, and sites of
RT	synthesis."
RL	J. Biol. Chem. 264:5957-5965(1989).
CC	-1- FUNCTION: Plasmin dissolves the fibrin of blood clots and acts as
CC	a proteolytic factor in a variety of other processes including
CC	embryonic development, tissue remodeling, tumor invasion, and
CC	inflammation; in ovulation it weakens the walls of the Graafian
CC	follicle. It activates the urokinase-type plasminogen activator,
CC	collagenases and several complement zymogens, such as C1 and C5.
CC	It cleaves fibrin, fibronectin, thrombospondin, laminin and von
CC	Willebrand factor.
CC	-1- CATALYTIC ACTIVITY: Preferential cleavage: Lys -Xaa > Arg -Xaa;
CC	higher selectivity than trypsin. Converts fibrin into soluble
CC	products.
CC	-1- ENZYME REGULATION: Converted into plasmin by plasminogen
CC	activators, both plasminogen and its activator being bound to
CC	fibrin. Activated with catalytic amounts of streptokinase.
CC	-1- SUBCELLULAR LOCATION: Secreted.
CC	-1- MISCELLANEOUS: Plasmin is inactivated by alpha-2-antiplasmin
CC	immediately after dissociation from the clot.
CC	-1- MISCELLANEOUS: In the presence of the inhibitor, the activation
CC	involves net cleavage after Arg-580, resulting in 2 chains held
CC	together by 2 disulfide bonds. Without the inhibitor, the
CC	activation involves also removal of the activation peptide.
CC	-1- SIMILARITY: Belongs to the peptidase S1 family. Plasminogen
CC	subfamily.
CC	-1- SIMILARITY: Contains 5 kringle domains.

CC	-1- SIMILARITY: Contains 1 PAN domain.
CC	-----
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration
CC	between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC	the European Bioinformatics Institute. There are no restrictions on its
CC	use by non-profit institutions as long as its content is in no way
CC	modified and this statement is not removed. Usage by and for commercial
CC	entities requires a license agreement (See <a href="http://www.isdb-bib.ch/announce/">http://www.isdb-bib.ch/announce/</a>
CC	or send an email to <a href="mailto:license@isdb-bib.ch">license@isdb-bib.ch</a> ).
CC	-----
DR	EMBL; J04697; AAA6901.1; -
DR	PIR; B32869; B30848.
DR	HSSP; P00747; IBUI.
DR	MEROPS; S01_233; -
DR	InterPro; IPR000001; Kringle.
DR	InterPro; IPR003014; PAN.
DR	InterPro; IPR003609; Pan app.
DR	InterPro; IPR009003; Pept Ser Cys.
DR	InterPro; IPR001254; Peptidase \$I\$.
DR	InterPro; IPR001314; Peptidase \$II\$.
DR	InterPro; IPR003966; Peptidase \$III_a\$ pr.
DR	Pfam; PF000051; Kringle; 5.
DR	Pfam; PF00024; PAN; 1.
DR	Pfam; PF00089; Trypsin; 1.
DR	PIRSEF; PIRSF001150; Plasmin; 1.
DR	PRINTS; PR00722; CHYMOTRYPSIN.
DR	PRINTS; PR00018; KRINGLE.
DR	PRINTS; PR01505; PROTHROMBIN.
DR	Prodom; PD000395; Kringle; 5.
DR	SMART; SMO0130; KR; 5.
DR	SMART; SMO0473; PAN Ap; 1.
DR	SMART; SMO0020; TRY_Psp; 1.
DR	PROSITE; PS00021; KRINGLE_1; 5.
DR	PROSITE; PS50070; KRINGLE_2; 5.
DR	PROSITE; PS50948; PAN; 1.
DR	PROSITE; PS50240; TRYPsin DOM; 1.
DR	PROSITE; PS00134; TRYPsin_HIS; 1.
DR	PROSITE; PS00135; TRYPsin_SER; 1.
KW	Blood coagulation; Fibrinolysis; Glycoprotein; Hydrolase; Kringle;
KW	Plasma; Repeat; Serine protease; Signal; Tissue remodeling; Zymogen.
KM	SIGNAL 1 19
FT	CHAIN 20 810 plasminogen.
FT	CHAIN 20 580 plasmin heavy chain A.
FT	PEPTIDE 20 96 Activation peptide.
FT	CHAIN 97 580 Plasmin short form of chain A.
FT	CHAIN 581 810 Plasmin light chain B.
FT	DOMAIN 20 98 PAN.
FT	DOMAIN 103 181 Kringle 1.
FT	DOMAIN 184 262 Kringle 2.
FT	DOMAIN 275 352 Kringle 3.
FT	DOMAIN 377 454 Kringle 4.
FT	DOMAIN 481 560 Kringle 5.
FT	DOMAIN 581 810 Serine protease.
FT	ACT_SITE 622 Charge relay system.
FT	ACT_SITE 665 Charge relay system.
FT	ACT_SITE 760 Charge relay system.
FT	BINDING 136 136 Omega-amino-carboxylic acids.
FT	BINDING 158 158 Omega-amino-carboxylic acids.
FT	BINDING 172 172 Omega-amino-carboxylic acids.
FT	BINDING 432 432 Omega-amino-carboxylic acids.
FT	BINDING 445 445 Omega-amino-carboxylic acids.
FT	BINDING 134 134 Fibrin.
FT	BINDING 136 136 Fibrin.
FT	DISULFID 49 73 By similarity.
FT	DISULFID 53 61 By similarity.
FT	DISULFID 103 181 By similarity.
FT	DISULFID 124 164 By similarity.
FT	DISULFID 152 176 By similarity.
FT	DISULFID 185 262 By similarity.
FT	DISULFID 316 316 By similarity.
FT	DISULFID 206 245 By similarity.
FT	DISULFID 234 257 By similarity.
FT	DISULFID 275 352 By similarity.

FT DISULFID 296 335 By similarity.  
 FT DISULFID 324 347 By similarity.  
 FT DISULFID 377 454 By similarity.  
 FT DISULFID 398 437 By similarity.  
 FT DISULFID 426 449 By similarity.  
 FT DISULFID 481 560 By similarity.  
 FT DISULFID 502 543 By similarity.  
 FT DISULFID 531 555 By similarity.  
 FT DISULFID 567 685 Interchain (By similarity).  
 FT DISULFID 577 585 Interchain (By similarity).  
 FT DISULFID 607 623 By similarity.  
 FT DISULFID 699 766 By similarity.  
 FT DISULFID 729 745 By similarity.  
 FT DISULFID 756 784 By similarity.  
 FT CARBOHYD 365 365 O-linked (GlcNAc...) (By similarity).  
 SQ SEQUENCE 810 AA; 90255 MW; A75E1C51A1A0F24A CRC64;

Query Match 93.6%; Score 1442; DB 1; Length 810;  
 Best Local Similarity 93.1%; Pred. No. 1.3e-101;  
 Matches 242; Conservative 9; Mismatches 9; Indels 0; Gaps 0;

QY 1 VYLSECTGNGKNGKRGTMSTKNGITCOKWSSTSPHPRPSPATHPSEGLEENYCRNPDN 60  
 |||||  
 DB 98 VYLSECTGNGKNGKRGTMSTKNGITCOKWSSTSPHPRPSPATHPSEGLEENYCRNPDN 157  
 |||||

QY 61 DPGPMCTTDPPEKRYDYCDILECEECMHCSENGYDGIKSTKMSGLECOAMDSPH 120  
 |||||  
 DB 158 DPGPMCTTDPPEKRYDYCDILECEECMHCSENGYDGIKSTKMSGLECOAMDSPH 217  
 |||||

QY 121 GIYPSKFPKNIKKNYCRNPDRELPRWCFTTDPNKNWELCDIPRCTPPSSGPTTQC 180  
 |||||  
 DB 218 GIYPSKFPKNIKKNYCRNPDRELPRWCFTTDPNKNWELCDIPRCTPPSSGPTTQC 277  
 |||||

QY 181 GTGENYRGNAVTVSGHTCOHWSAOTPHRTPEPNPCNDENYCRNPDGKRAPWCHT 240  
 |||||  
 DB 278 GTGENYRGNAVTVSGHTCOHWSAOTPHRTPEPNPCNDENYCRNPDGKRAPWCHT 337  
 |||||

QY 241 TNSQVRWEYCKIPSCDSSPV 260  
 |||||  
 DB 338 TNSQVRWEYCKIPSCDSSPV 357  
 |||||

RESULT 3  
 Q8WMR1 PRELIMINARY; PRT; 359 AA.  
 ID Q8WMR1;  
 AC Q8WMR1;  
 DT 01-MAR-2002 (Tremblrel. 20, Created)  
 DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)  
 DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)  
 DE Plasmalogen (Fragment).  
 DE Canis familiaris (Dog).  
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
 NX NCBI\_Taxid=9615;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Pille-Shepherd S.R., Coffman K.T., Resnick D., Chan R., Kisker O.,  
 RA Folkman J., Waters D.J.;  
 RL Submitted (DEC-2001) to the EMBL/Genbank/DBJ databases.  
 DR EMBL: AY069985; AAL58519.1;  
 DR HSRP; P00747; IPWK.  
 DR GO; GO:0005509; F:calcium ion binding; IEA.  
 DR GO; GO:0003809; F:thrombin activity; IEA.  
 DR GO; GO:0007596; P:blood coagulation; IEA.  
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.  
 DR Pfam; PF00051; Kringle\_4.  
 DR PRINTS; PRO0018; KRINGLE\_4.  
 DR PRINTS; PRO1505; PROTHROMBIN.  
 DR PRODOM; PD000395; Kringle\_4.  
 DR SMART; SM00130; KR; 4.  
 DR PROSITE; PS00021; KRINGLE\_1; 4.  
 DR PROSITE; PS00070; KRINGLE\_2; 4.  
 KW Kringle.

FT NON TER 1 1  
 FT NON TER 359 359  
 SQ SEQUENCE 359 AA; 41172 MW; 776D35F4AB0BD9E CRC64;

Query Match 84.8%; Score 1306; DB 2; Length 359;  
 Best Local Similarity 81.2%; Pred. No. 1.3e-91;  
 Matches 211; Conservative 23; Mismatches 26; Indels 0; Gaps 0;

QY 1 VYLSECTGNGKNGKRGTMSTKNGITCOKWSSTSPHPRPSPATHPSEGLEENYCRNPDN 60  
 |||||  
 DB 1 VYLSECTGNGKNGKRGTMSTKNGITCOKWSSTSPHPRPSPATHPSEGLEENYCRNPDN 60  
 |||||

QY 61 DPGPMCTTDPPEKRYDYCDILECEECMHCSENGYDGIKSTKMSGLECOAMDSPH 120  
 |||||  
 DB 61 DPGPMCTTDPPEKRYDYCDILECEECMHCSENGYDGIKSTKMSGLECOAMDSPH 120  
 |||||

QY 121 GIYPSKFPKNIKKNYCRNPDRELPRWCFTTDPNKNWELCDIPRCTPPSSGPTTQC 180  
 |||||  
 DB 121 GIYPSKFPKNIKKNYCRNPDRELPRWCFTTDPNKNWELCDIPRCTPPSSGPTTQC 180  
 |||||

QY 181 GTGENYRGNAVTVSGHTCOHWSAOTPHRTPEPNPCNDENYCRNPDGKRAPWCHT 240  
 |||||  
 DB 181 GTGENYRGNAVTVSGHTCOHWSAOTPHRTPEPNPCNDENYCRNPDGKRAPWCHT 240  
 |||||

QY 241 TNSQVRWEYCKIPSCDSSPV 260  
 |||||  
 DB 241 TNSQVRWEYCKIPSCDSSPV 260  
 |||||

RESULT 4  
 PLMN RAT STANDARD; PRT; 812 AA.  
 ID PLMN RAT  
 AC 00117; O9ROW3;  
 DT 01-APR-1993 (Rel. 25, Created)  
 DT 25-OCT-2004 (Rel. 45, Last sequence update)  
 DT 25-OCT-2004 (Rel. 45, Last annotation update)  
 DE Plasmalogen precursor (EC 3.4.21.7) [Contains: Angiotensin].  
 GN Name:Plg;  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 NX NCBI\_Taxid=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Tissue=Liver;  
 RC Tissue=Liver;  
 RA Bangert K., Johnsen A.H., Thorsen S.;  
 RL "Rat plasminogen: cDNA and gene structure."  
 RL Submitted (MAY-1999) to the EMBL/Genbank/DBJ databases.  
 RN [2]  
 RP SEQUENCE OF 343-511 FROM N.A.  
 RC Tissue=Liver;  
 RX MEDLINE=91250378; PubMed=1645711;  
 RA Kanalas J.J., Makler S.P.;  
 RL "Identification of the rat Heymann nephritis autoantigen (GP330) as a  
 RT receptor site for plasminogen."  
 RL J. Biol. Chem. 266:10825-10829(1991).  
 CC -1- FUNCTION: Plasmin dissolves the fibrin of blood clots and acts as  
 CC a proteolytic factor in a variety of other processes including  
 CC embryonic development, tissue remodeling, tumor invasion, and  
 CC inflammation; in ovulation it weakens the walls of the Graafian  
 CC follicle. It activates the urokinase-type plasminogen activator,  
 CC collagenases and several complement zymogens, such as C1 and C5.  
 CC It cleaves fibrin, fibronectin, thrombospondin, laminin and von  
 CC Willebrand factor.  
 CC -1- FUNCTION: Angiotensin is an angiogenesis inhibitor that blocks  
 CC neovascularization and growth of experimental primary and  
 CC metastatic tumors in vivo (By similarity).  
 CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Lys-|-Xaa > Arg-|-Xaa;  
 CC higher selectivity than trypsin. Converts fibrin into soluble  
 CC products.  
 CC -1- ENZYME REGULATION: Converted into plasmin by plasminogen  
 CC activators, both plasminogen and its activator being bound to  
 CC fibrin. Cannot be activated with streptokinase.

Query Match	Best Local Similarity	84.4%; Score 1299; DB 1; Length 812;
Matches 213; Conservative 21; Mismatches 24; Indels 0; Gaps 0;		
QY 1 VYLSECTGKGNKRYGKMTSTNGITGTCQKSSSTSPHPRPRSSPATHPSEGLBNYCRPNP 60	124 164 By similarity.	
DB 98 VYLSECTGKIGKGRGMSKTKGVTQCKMSDTSPHVFKXSPSTHPSEGLEBNYCRPNP 157	152 176 By similarity.	
QY 61 DPGPMCTCTDPEKRYDYCDILECEECEHCMSGENYDGKISTKMSGLECOAMPDSPPAH 120	185 262 By similarity.	
DB 158 DEGPQWCTTDDPDQRYRYTCNIPCEBECMCYCSGKTKBGKISKTMGSLDCCMSQSPAH 217	188 245 By similarity.	
QY 121 GYIPSKFPNNLKNKCRNPDRRLPWCFTTDPNKKWELCDIPRCTTPPPSSGPTYQCLK 180	206 245 By similarity.	
DB 218 GYIPAKFPKNNLKNKCRNPDRRLPWCFTTDPNKKWELCDIPRCTTPPPSSGPTYQCLK 277	234 257 By similarity.	
QY 181 GTCENTRGNAVYVSGHTCQHNAAQPHHTERKTPENFPCCNLBNYCRNPDGKRAPWCHT 240	275 352 By similarity.	
DB 278 GRCNRYGTVSVASGTCQRMSEQTPHRNKRTPENFPCCNLBNYCRNPDGTAIPWCYT 337	296 335 By similarity.	
QY 241 TNSQVMEYCKIPSCDS 258	324 347 By similarity.	
DB 338 TDSQVMEYCKIPSCGS 355	376 454 By similarity.	
	397 437 By similarity.	
	425 449 By similarity.	
	481 560 By similarity.	
	502 543 By similarity.	
	531 555 By similarity.	
	568 687 Interchain (By similarity).	
	578 586 Interchain (By similarity).	
	609 625 By similarity.	
	701 768 By similarity.	
	731 747 By similarity.	
	758 786 By similarity.	
	418 418 A -> S (in Ref. 2).	
SO SEQUENCE 812 AA; 90535 MM; 8C703C51410BCE CRC64;		



RT "Determination of the complete amino-acid sequence of porcine miniplasminogen." Eur. J. Biochem. 149:279-285 (1985).

RT (3)

RP CARBOHYDRATE-LINKAGE SITES.

RX MEDLINE=88185329; PubMed=3356193;

RA Mari T., Schaller J., Rickli E.E., Schmid K., Kamerling J.P., Gerwig G.J., van Halbeek H., Vilegenthart J.F.; "The N- and O-linked carbohydrate chains of human, bovine and porcine plasminogen. Species specificity in relation to sialylation and fucosylation patterns." Eur. J. Biochem. 173:57-63 (1988).

CC -1- FUNCTION: Plasmin dissolves the fibrin of blood clots and acts as a proteolytic factor in a variety of other processes including embryonic development, tissue remodeling, tumor invasion, and inflammation; in ovulation it weakens the walls of the Graafian follicle. It activates the urokinase-type plasminogen activator, collagenases and several complement zymogens, such as C1 and C5. It cleaves fibrin, fibronectin, thrombospondin, laminin and von Willebrand factor.

CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Lys-|-Xaa > Arg-|-Xaa; higher selectivity than trypsin. Converts fibrin into soluble products.

CC -1- ENZYME REGULATION: Converted into plasmin by plasminogen activators, both plasminogen and its activator being bound to fibrin. Cannot be activated with streptokinase.

CC -1- SUBCELLULAR LOCATION: Secreted.

CC -1- PTM: N-linked glycan contains N-acetylglucosamine, sialic acid and disaccharide which is modified with up to 2 sialic residues (microheterogeneity).

CC -1- MISCELLANEOUS: Plasmin is inactivated by alpha-2-antiplasmin immediately after dissociation from the clot.

CC -1- SIMILARITY: Belongs to the peptidase S1 family. Plasminogen subfamily.

CC -1- SIMILARITY: Contains 5 kringle domains.

CC -1- SIMILARITY: Contains 1 PAN domain.

DR HSSP: P00747; PLPG.

DR MEROPS: S01.233; -.

DR GlycoSiteDB: P06867; -.

DR InterPro: IPR000001; Kringle.

DR InterPro: IPR003014; PAN.

DR InterPro: IPR003609; Pan\_APP.

DR InterPro: IPR001254; Peptidase\_S1.

DR InterPro: IPR001314; Peptidase\_S1A.

DR InterPro: IPR003966; Peptidase\_S1A\_pr.

DR InterPro: IPR009003; Pept\_Ser\_Cys.

DR Pfam: PF00051; Kringle; 5.

DR Pfam: PF00024; PAN; 1.

DR PIRSF: PIRSF001150; Plasmin; 1.

DR PRINTS: PR00722; CHYMOTRYPSIN.

DR PRINTS: PR00018; KRINGLE.

DR PRINTS: PR01505; PROTHROMBIN.

DR ProDom: PD000395; Kringle; 5.

DR SMART: SM00130; KR; 5.

DR SMART: SM00473; PAN\_AP; 1.

DR SMART: SM00020; Tryp\_Spc; 1.

DR PROSITE: PS00021; KRINGLE\_1; 5.

DR PROSITE: PS00070; KRINGLE\_2; 5.

DR PROSITE: PS50948; PAN; 1.

DR PROSITE: PS50240; TRYPSIN\_DOM; 1.

DR PROSITE: PS00134; TRYPSIN\_HIS; FALSE\_NEG.

DR PROSITE: PS00135; TRYPSIN\_SER; 1.

KM Blood coagulation; Direct protein sequencing; Fibrinolysis; Glycoprotein; Hydrolase; Kringle; Plasma; Repeat; Serine protease; Tissue remodeling; Zymogen.

FT CHAIN 1 560 Plasmin heavy chain A.

FT CHAIN 561 790 Plasmin light chain B.

FT DOMAIN 1 79 PAN.

FT DOMAIN 561 790 Serine protease.

FT DOMAIN 84 162 Kringle 1.

FT DOMAIN 166 243 Kringle 2.

FT DOMAIN 256 333 Kringle 3.

FT DOMAIN 358 435 Kringle 4.

FT DOMAIN 461 540 Kringle 5.

FT ACT\_SITE 602 602 Charge relay system.

FT ACT\_SITE 645 645 Charge relay system.

FT ACT\_SITE 740 740 Charge relay system.

FT CARBOHYD 289 289 N-linked (GlcNAc...).

FT CARBOHYD 340 340 O-linked (GalNAc...).

FT SEQUENCE 790 AA; 88592 MW; F04BA06E74BCD58E CRC64;

Query Match 83.9%; Score 1292; DB 1; Length 790;

Best Local Similarity 81.4%; Pred. No. 3 4e-90;

Matches 210; Conservative 23; Mismatches 25; Indels 0; Gaps 0;

Qy 1 VYLSECKTGNGKNYRGTMSKTKNGITCKMSSTSPRRPFPSPATHPSEGLEENYCNPN 60

Db 79 IYLSECKTGNGKNYRGTSTKSGVLCQKWSVSPHLPKSPKPLAGLEENYCNPN 138

Qy 61 DPGPMCTTDPKRYDYCDILEECCHGSGENTDKISKTMGLCOAMDSPHAY 120

Db 139 DEKPMCTTDPETRDYCDIPECDECHGSGEHYEGKISKTMGIECOSWGSOPHAY 198

Qy 121 GYIPSKFPNNKLNKKNYCNPNDRPWCFTTDPNKKWELCDIPRCTTTPPSGPTQCLK 180

Db 199 GYIPSKFPNNKLNKKNYCNPNDRPWCFTTDPNKKWELCDIPRCTTTPPSGPTQCLK 258

Qy 181 GTGENRYGNVAVTVSQHTCOHWSAQTPHTERTPENPCKNLDENYCNPNDRGAPWCHT 240

Db 259 GRENRGVTYSVASHTCOHWSAQSPHNNRPENPCKNLEENYCNPNDRGTAWCT 318

Qy 241 TNSQVMEYCKIPSCSS 258

Db 319 TDSVEMDYCKIPSCSS 336

RESULT 6

PLAN\_BOVIN STANDARD; PRT; 812 AA.

ID P06868; Q28162;

DT 01-JAN-1988 (Rel. 06, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 25-OCT-2004 (Rel. 45, Last annotation update)

DE Plasminogen precursor (EC 3.4.21.7).

GN Name=PLG;

OS Bos taurus (Bovine).

OC Chordata; Craniata; Vertebrata; Euteleostomi;

OC Eukaryota; Metazoa; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

OX NCBI\_TaxID=9913;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Liver;

RA Berglund L., Andersen M.D., Petersen T.E.;

RT "Cloning and characterization of the bovine plasminogen cDNA.";

RL Int. Dairy J. 5:593-603 (1995).

RN [2]

RP SEQUENCE OF 27-812, AND CARBOHYDRATE-LINKAGE SITES.

RX MEDLINE=85203906; PubMed=3846532;

RA Schaller J., Moser P.W., Danneberg-Muller G.A.K., Rosseler S.J., Kamper U., Rickli E.E.;

RT "Complete amino acid sequence of bovine plasminogen. Comparison with human plasminogen." Eur. J. Biochem. 149:267-278 (1985).

RL Eur. J. Biochem. 149:267-278 (1985).

RN [3]

RP SEQUENCE OF 706-812 FROM N.A.

RX MEDLINE=85023311; PubMed=6148961;

RA Malinowski D.P., Sadler J.E., Davie E.W.;

RT "Characterization of a complementary deoxyribonucleic acid coding for human and bovine plasminogen." Biochemistry 23:4243-4250 (1984).

[4]

RP CARBOHYDRATE-LINKAGE SITES.

RX MEDLINE=66185329; PubMed=3356193;

RA Marti T., Schallier J., Rickli E.E., Schmid K., Kamerling J.P.,

RV Gerwig G.J., van Halbeek H., Vliegenhart J.P.;

RT "The N- and O-linked carbohydrate chains of human, bovine and porcine

RT plasminogen. Species specificity in relation to sialylation and

RT fucosylation patterns".

RL Eur. J. Biochem. 173:57-63(1988).

CC -1- FUNCTION: Plasmin dissolves the fibrin of blood clots and acts as

CC a proteolytic factor in a variety of other processes including

CC embryonic development, tissue remodeling, tumor invasion, and

CC inflammation; in ovulation it weakens the walls of the Graafian

CC follicle. It activates the urokinase-type plasminogen activator,

CC collagenases and several complement zymogens, such as C1 and C5.

CC It cleaves fibrin, fibronectin, thrombospondin, laminin and von

CC Willebrand factor.

CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Lys-|-Xaa > Arg-|-Xaa;

CC higher selectivity than trypsin. Converts fibrin into soluble

CC products.

CC -1- ENZYME REGULATION: Converted into plasmin by plasminogen

CC activators, both plasminogen and its activator being bound to

CC fibrin. Cannot be activated with streptokinase.

CC -1- SUBCELLULAR LOCATION: Secreted.

CC -1- PM: N-linked glycan contains N-acetylglucosamine and sialic acid.

CC O-linked glycans consist of Gal-GalNAc disaccharide which is

CC modified with up to 2 sialic acid residues (microheterogeneity).

CC -1- MISCELLANEOUS: Plasmin is inactivated by alpha-2-antiplasmin

CC immediately after dissociation from the clot.

CC -1- SIMILARITY: Belongs to the peptidase S1 family. Plasminogen

CC subfamily.

CC -1- SIMILARITY: Contains 5 kringle domains.

CC -1- SIMILARITY: Contains 1 PAN domain.

CC -----

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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC the European Bioinformatics Institute. There are no restrictions on its

CC use by non-profit institutions as long as its content is in no way

CC modified and this statement is not removed. Usage by and for commercial

CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>

CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).

CC -----

DR EMBL; X79602; CAA55939.1; -

DR EMBL; K02935; AAB30714.1; -

DR PIR; S45046; PLBO.

DR HSSP; P00747; 2PKA.

DR MEROPS; S01.233; -

DR GlycoSuiteDB; P06868; -

DR InterPro; IPR000001; Kringle.

DR InterPro; IPR003014; PAN.

DR InterPro; IPR009003; Pept\_Ser\_Cys.

DR InterPro; IPR001254; Peptidase\_S1.

DR InterPro; IPR001314; Peptidase\_S1A.

DR InterPro; IPR003966; Peptidase\_S1A\_pr.

DR Pfam; PF00051; Kringle; 5.

DR Pfam; PF00024; PAN; 1.

DR Pfam; PF00089; Trypsin; 1.

DR PIRSF; PIRSF001150; Plasmin; 1.

DR PRINTS; PR00722; CHYMOTRYPSIN.

DR PRINTS; PR00018; KRINGLE.

DR PRINTS; PR01505; PROTHROMBIN.

DR ProDom; PD000395; Kringle; 5.

DR ProSITE; PS00021; KRINGLE\_1; 5.

DR ProSITE; PS50070; KRINGLE\_2; 5.

DR ProSITE; PS50948; PAN; 1

DR PROSITE; PS50240; TRYPSIN\_DOM; 1.

DR PROSITE; PS00134; TRYPSIN\_HIS; 1.

DR PROSITE; PS00135; TRYPSIN\_SER; 1.

RV Blood coagulation: Direct protein sequencing; Fibrinolysis;

RV Glycoprotein: Hydrolyase; Kringle; Plasma; Repeat; Serine protease;

RV Signal; Tissue remodeling; Zymogen.

FT SIGNAL 1 26

FT CHAIN 27 812 Plasminogen.

FT	CHAIN	27	583	Plasma heavy chain A.
FT	CHAIN	584	812	Plasma light chain B.
FT	DOMAIN	29	105	PAN.
FT	DOMAIN	110	188	Kringle 1.
FT	DOMAIN	192	269	Kringle 2.
FT	DOMAIN	282	359	Kringle 3.
FT	DOMAIN	384	461	Kringle 4.
FT	DOMAIN	485	564	Kringle 5.
FT	CARBOHYD	584	812	Serine protease.
FT	CARBOHYD	315	315	N-linked (G1CNAC. . .).
FT	CARBOHYD	365	365	O-linked (GALNAc. . .).
FT	ACT_SITE	624	624	/FTID=CAR.000015.
FT	ACT_SITE	667	667	Charge relay system.
FT	ACT_SITE	762	762	Charge relay system.
FT	CONFLICT	335	335	N -> D (in Ref. 2).
FT	CONFLICT	516	516	O -> H (in Ref. 2).
FT	CONFLICT	555	555	P -> L (in Ref. 2).
FT	CONFLICT	744	744	T -> R (in Ref. 3).
SO	SEQUENCE	812 AA;	91216 MW;	386AA691E220946 CRC64;
Query Match				
Best Local Similarity 80.8%; Score 1291; DB 1; Length 812;				
Matches 210; Conservative 23; Mismatches 27; Indels 0; Gaps 0				
Qy	1	VTLECKTGNGKNYGTMSKTKNGITTCQKMSSTSPHRRFPSPATHPSGLSEENYCRNPDN	60	
Db	105	VTLECKTGNGQYRTAETKSGVTCQKMSATSPHYVFKSPKRPPLAGLEENYCRNPDN	164	
Qy	61	DPOSPCCTTDPKRYDYCDLLEEEBCNHCSSGENYDCKISKITMSGLECOAWDSQSPHAA	120	
Db	165	DENPMPCTTDPDKRYDYCDLLEEEBCNHCSSGENYDCKISKITMSGLECOAWDSQSPHAA	224	
Qy	121	GYIPSKCPNNKLNKNYGRNPNRELPMPCFTTDPKRWELCDIPCTTPPSAGPTYYCCK	180	
Db	225	GYIPSKCPNNKLNKNYGRNPNRELPMPCFTTDPKRWELCDIPCTTPPSAGPTYYCCK	284	
Qy	181	GTGENTYRGNAVTVYSGHTCQMSAQTPTHTERTENFPCKULDENYCRNPDGKRAPWCHT	240	
Db	285	GTGKNYGVYAVVIESGHTCQMSQTHKKNRTENFPCKULDENYCRNPDGKRAPWCHT	344	
Qy	241	TNSQVMEYCKIPSCDSSPV	260	
Db	345	TNSEVMEYCTIPSCDSSPV	364	
RESULT 7				
Q6TC10 PRELIMINARY; PRT; 466 AA.				
DT	05-JUL-2004	(TREMBLrel. 27, Created)		
DT	05-JUL-2004	(TREMBLrel. 27, Last sequence update)		
DT	05-JUL-2004	(TREMBLrel. 27, Last annotation update)		
OS	Mus musculus	(Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=Kunming;			
RA	Giao H., Tang B., Sun X.;			
RL	Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AY424276; AAR07361.1; -.			
DR	HSSP; P00747; I821.			
DR	GO; GO:0005615; C:extracellular space; TAS.			
DR	GO; GO:0006915; P:apoptosis; IDA.			
DR	GO; GO:0006917; P:induction of apoptosis; IDA.			
DR	GO; GO:0046716; P:muscle maintenance; IMP.			
DR	GO; GO:0007519; P:myogenesis; IMP.			
DR	GO; GO:0016525; P:negative regulation of angiogenesis; TAS.			
DR	GO; GO:0042246; P:tissue regeneration; IMP.			

DR InterPro; IPR000001; Kringle.  
 DR InterPro; IPR003014; PAN.  
 DR InterPro; IPR003609; PAN\_APP.  
 DR InterPro; IPR003966; Peptidase\_S1A\_pr.  
 DR InterPro; IPR001400; Somatotropin.  
 DR Pfam; PF00051; Kringle; 4.  
 DR Pfam; PF00024; PAN; 1.  
 DR PRINTS; PR00018; KRINGLE.  
 DR PRINTS; PR01505; PROTHROMBIN.  
 DR ProDom; PD000395; Kringle; 4.  
 DR SMART; SM00130; KR; 4.  
 DR SMART; SM00473; PAN\_AP; 1.  
 DR PROSITE; PS00021; KRINGLE\_1; 4.  
 DR PROSITE; PS00070; KRINGLE\_2; 4.  
 DR PROSITE; PS00948; PAN; 1.  
 DR PROSITE; PS00338; SOMATOTROPIN\_2; UNKNOWN\_1.  
 DR Kringle.  
 KW Kringle.  
 SQ SEQUENCE 466 AA; 52717 MW; 3ED3298C34C39116 CRC64;  
 Query Match 83.1%; Score 1279; DB 2; Length 466;  
 Best Local Similarity 81.0%; Pred. No. 1.9e-89;  
 Matches 209; Conservative 22; Mismatches 27; Indels 0; Gaps 0;  
 QY 1 VYLSECKTGNGKNGKNGSKTNGITTCQKMSSTSPHPRFSPDATHPSGLEENTCRNPDN 60  
 DB 98 VYLSECKTGNGKNGKNGSKTNGITTCQKMSSTSPHPRFSPDATHPSGLEENTCRNPDN 157  
 QY 61 DPGKWCCTTDPKRYDNCNPECEBECMYSGEKYBKISKTSGLDCCQAMDSQSPH 120  
 DB 158 DPGKWCCTTDPKRYDNCNPECEBECMYSGEKYBKISKTSGLDCCQAMDSQSPH 217  
 QY 121 GYIPSPKPNKULKNVYCNPNPRELPMCFCTTDPNRMELCDIPCTTTPPPSSGPTYOCLK 180  
 DB 218 GYIPSPKPNKULKNVYCNPNPRELPMCFCTTDPNRMELCDIPCTTTPPPSSGPTYOCLK 277  
 QY 181 GTGNGRNVAVYVTSQHTCQMSAOTPTHTERTPNPCKULDENYCNPDGKAPWCHT 240  
 DB 278 GTGNGRNVAVYVTSQHTCQMSAOTPTHTERTPNPCKULDENYCNPDGKAPWCHT 337  
 QY 241 TNSGVNWEYCKIPSCDSS 258  
 DB 338 TDSQRMWEYCEIPSCSS 355  
 RESULT 8  
 PLAN\_MOUSE  
 ID PLAN\_MOUSE STANDARD; PRT; 812 AA.  
 AC P20918; O8C1S2; O91W05;  
 DT 01-FEB-1991 (Rel. 17, Created)  
 DT 10-OCT-2003 (Rel. 42, Last sequence update)  
 DT 25-OCT-2004 (Rel. 45, Last annotation update)  
 DE Plasminogen precursor (EC 3.4.21.7) [Contains: Angiostatin].  
 GN Name=Plg;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=91184812; PubMed=2081600;  
 RA Degen S.V., Bell S.W., Schaefer L.A., Elliott R.W.;  
 RT "Characterization of the cDNA coding for mouse plasminogen and  
 RT localization of the gene to mouse chromosome 17.";  
 RL Genomics 8:49-61(1990).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX STRAIN=129/Sv;  
 RA Brathwaite M., waeltz P., Qian Y., Dudekula D., Schlessinger D.,  
 RA Nagaraja R.;  
 RT "Genomic sequence analysis in the mouse t-complex region.";  
 RL Submitted (Feb-2002) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.

RC TISSUE=Liver;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Straussberg R.L., Feigold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schaller G.D.,  
 RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Maruska K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Ustin T.B., Toehlyuk S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
 RA Bosak S.A., McSwan P.J., McKernan K.J., Malek U.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hultk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Pahey J., Helton E., Ketterman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [4]  
 RP SEQUENCE OF 1-16 FROM N.A.  
 RX STRAIN=129/Sv; TISSUE=Liver;  
 RA PubMed=12149246; DOI=10.1074/jbc.M202809200;  
 RA Bannach F.G., Gutierrez A., Fowler B.J., Bugge T.H., Degen J.L.,  
 RA Farmer R.J., Miles L.A.;  
 RT "Localization of regulatory elements mediating constitutive and  
 RT cytokine-stimulated plasminogen gene expression.";  
 RL J. Biol. Chem. 277:38579-38588(2002).  
 RN [5]  
 RP CHARACTERIZATION OF ANGIOSTATIN, AND PARTIAL SEQUENCE.  
 RX MEDLINE=95042728; PubMed=7525077; DOI=10.1016/0092-8674(94)90200-3;  
 RA O'Reilly M.S., Holmgren L., Shing Y., Chen C., Rosenthal R.A.,  
 RA Moses M., Lane W.S., Cao Y., Sage E.H., Folkman J.;  
 RT "Angiostatin: a novel angiogenesis inhibitor that mediates the  
 RT suppression of metastases by a Lewis lung carcinoma.";  
 RL Cell 79:315-328(1994).  
 CC -1- FUNCTION: Plasmin dissolves the fibrin of blood clots and acts as  
 CC a proteolytic factor in a variety of other processes including  
 CC embryonic development, tissue remodeling, tumor invasion, and  
 CC inflammation; in ovulation it weakens the walls of the Graafian  
 CC follicle. It activates the urokinase-type plasminogen activator,  
 CC collagenases and several complement zymogens, such as C1 and C5.  
 CC It cleaves fibrin, fibronectin, thrombospondin, laminin and von  
 CC Willebrand factor.  
 CC -1- FUNCTION: Angiostatin is an angiogenesis inhibitor that blocks  
 CC neovascularization and growth of experimental primary and  
 CC metastatic tumors in vivo.  
 CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Lys-|-Xaa > Arg-|-Xaa;  
 CC higher selectivity than trypsin. Converts fibrin into soluble  
 CC products.  
 CC -1- ENZYME REGULATION: Converted into plasmin by plasminogen  
 CC activators, both plasminogen and its activator being bound to  
 CC fibrin. Cannot be activated with streptokinase.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- MISCELLANEOUS: Plasmin is inactivated by alpha-2-antiplasmin  
 CC immediately after dissociation from the clot.  
 CC -1- INVOLVES: In the presence of the inhibitor, the activation  
 CC involves only cleavage after Arg-581, resulting in 2 chains held  
 CC together by 2 disulfide bonds. Without the inhibitor, the  
 CC activation involves also removal of the activation peptide.  
 CC -1- SIMILARITY: Belongs to the peptidase S1 family. Plasminogen  
 CC subfamily.  
 CC -1- SIMILARITY: Contains 5 kringle domains.  
 CC -1- SIMILARITY: Contains 1 PAN domain.  
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DR EMBL; J04766; AAA50168.1; -  
 DR EMBL; A0481053; AAM22156.1; -  
 DR EMBL; BC014773; AAM14773.1; -  
 DR EMBL; BC057186; AAM57186.1; -  
 DR EMBL; AY134430; AAM15805.1; -  
 DR PIR; A38514; PLMS.  
 DR HSSP; P00747; 1BUT.  
 DR MEROPS; S01.233; -  
 DR MGD; MGI.97620; P1g.  
 DR GO; GO:0006915; P:apoptosis; IDA.  
 DR GO; GO:0006917; P:induction of apoptosis; IDA.  
 DR InterPro; IPR000001; Kringle.  
 DR InterPro; IPR003014; PAN.  
 DR InterPro; IPR001254; Peptidase\_S1.  
 DR InterPro; IPR001314; Peptidase\_S1A.  
 DR InterPro; IPR003966; Peptidase\_S1A\_dr.  
 DR InterPro; IPR009003; Pept\_Ser\_Cys.  
 DR Pfam; PF00051; Kringle\_5.  
 DR Pfam; PF00024; PAN; 1.  
 DR Pfam; PF00089; Trypsin; 1.  
 DR PIRSF; PIRSF001150; Plasmin; 1.  
 DR PRINTS; PR00722; CHYMOTRYPSIN.  
 DR PRINTS; PR00018; KRINGLE.  
 DR PRINTS; PR01505; PROTHROMBIN.  
 DR Prodom; PD000395; Kringle; 5.  
 DR PROSITE; PS00021; KRINGLE\_1; 5.  
 DR PROSITE; PS50070; KRINGLE\_2; 5.  
 DR PROSITE; PS50948; PAN; 1.  
 DR PROSITE; PS50240; TRYPSIN\_DOM; 1.  
 DR PROSITE; PS00134; TRYPSIN\_HIS; 1.  
 DR PROSITE; PS00135; TRYPSIN\_SER; 1.  
 DR Blood coagulation; Direct protein sequencing; Fibrinolysis;  
 DR Glycoprotein; Hydrolyase; Kringle; Plasma; Repeat; Serine protease;  
 DR Signal; Tissue remodeling; Zymogen.  
 FT SIGNAL 1 19  
 FT CHAIN 20 812 Plasminogen.  
 FT CHAIN 20 581 Plasmin heavy chain A.  
 FT PEPTIDE 20 97 Activation peptide.  
 FT CHAIN 98 581 Plasmin short form of chain A.  
 FT CHAIN 98 7436 Angiotensin.  
 FT CHAIN 582 812 Plasmin light chain B.  
 FT DOMAIN 20 98 PAN.  
 FT DOMAIN 103 98 Kringle 1.  
 FT DOMAIN 184 262 Kringle 2.  
 FT DOMAIN 275 352 Kringle 3.  
 FT DOMAIN 377 454 Kringle 4.  
 FT DOMAIN 481 560 Kringle 5.  
 FT DOMAIN 582 812 Serine protease.  
 FT ACT\_SITE 624 624 Charge relay system (By similarity).  
 FT ACT\_SITE 667 667 Charge relay system (By similarity).  
 FT ACT\_SITE 762 762 Charge relay system (By similarity).  
 FT DISULFID 49 73 By similarity.  
 FT DISULFID 53 61 By similarity.  
 FT DISULFID 103 181 By similarity.  
 FT DISULFID 124 164 By similarity.  
 FT DISULFID 152 176 By similarity.  
 FT DISULFID 185 262 By similarity.  
 FT DISULFID 188 316 By similarity.  
 FT DISULFID 206 245 By similarity.  
 FT DISULFID 234 257 By similarity.  
 FT DISULFID 275 335 By similarity.  
 FT DISULFID 296 335 By similarity.  
 FT DISULFID 324 347 By similarity.  
 FT DISULFID 377 454 By similarity.  
 FT DISULFID 398 437 By similarity.  
 FT DISULFID 426 449 By similarity.  
 FT DISULFID 481 560 By similarity.  
 FT DISULFID 502 543 By similarity.  
 FT DISULFID 531 555 By similarity.  
 FT DISULFID 566 687 Interchain (By similarity).

FT DISULFID 578 586 Interchain (By similarity).  
 FT DISULFID 609 625 By similarity.  
 FT DISULFID 701 768 By similarity.  
 FT DISULFID 731 747 By similarity.  
 FT DISULFID 758 786 By similarity.  
 FT CONFLICT 235 235 R -> H (in Ref. 1).  
 FT CONFLICT 525 525 G -> D (in Ref. 1).  
 FT CONFLICT 649 649 S -> L (in Ref. 1).  
 SQ SEQUENCE 812 AA, 90781 MW, 24173260E6A2FFD2 CRC64;  
 Query Match 83.1%; Score 1279; DB 1; Length 812;  
 Best local similarity 81.0%; Pred. No. 3.5e-89;  
 Matches 209; Conservative 22; Mismatches 27; Indels 0; Gaps 0;  
 QY 1 VYLSECKTGNGKNYGTNSKTNGITTCQWMSSTSPHRRPSPATPSSGLEENYCRNPN 60  
 DB 98 VYLSECKTGNGKNYGTNSKTNGITTCQWMSSTSPHRRPSPATPSSGLEENYCRNPN 157  
 QY 61 DPGGWCCTTTPDKRYDTCDIIECEBECMGSGENYDCKISKTMSGLCQAWDSQSPAH 120  
 DB 158 DPGGWCCTTTPDKRYDTCNIPECEBECMGSGENYDCKISKTMSGLCQAWDSQSPAH 217  
 QY 121 GYIPKFPNKKYKKNYCNPNPRELPWCETTPDNKRWELCDIPRCTPPSSGPTVQCL 180  
 DB 218 GYIPKFPNKKYKKNYCNPNPRELPWCETTPDNKRWELCDIPRCTPPSSGPTVQCL 277  
 QY 181 GTGENYRGNAVTVSGHTCOHMSAQTPTHTERTPENPCCKULDENYCNPNPGKRAPWCHT 240  
 DB 278 GTGENYRGNAVTVSGHTCOHMSAQTPTHTERTPENPCCKULDENYCNPNPGKRAPWCHT 337  
 QY 241 TMSQVMEYCKIPSCDS 258  
 DB 338 TMSQVMEYCKIPSCDS 355  
 RESULT 9  
 PLNM ERIEU STANDARD; PRT; 810 AA.  
 ID PLNM ERIEU  
 AC Q29485;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 25-OCT-2004 (Rel. 45, Last annotation update)  
 DE Plasminogen precursor (EC 3.4.21.7).  
 GN Name=PLG;  
 OS Brinnaceus europaeus (Western European hedgehog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Insectivora; Brinnaceidae; Brinnaceinae; Brinnaceus.  
 OX NCBI\_Taxid=9365;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Liver;  
 RX MEDLINE=96025778; PubMed=7592597; DOI=10.1074/jbc.270.41.24004;  
 RA Lawn R.M., Boonmark N.W., Schwartz K., Lindahl G.B., Wade D.P.,  
 RA Byrne C.D., Fong K.J., Meer K., Patchy L.,  
 RT "The recurring evolution of lipoprotein(a). Insights from cloning of  
 RT hedgehog apolipoprotein(a)."  
 RT J. Biol. Chem. 270:24004-24009 (1995).  
 RP REVISIONS.  
 RA Lawn R.M.;  
 RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.  
 CC -!- FUNCTION: Plasmin dissolves the fibrin of blood clots and acts as  
 CC a proteolytic factor in a variety of other processes including  
 CC embryonic development, tissue remodeling, tumor invasion, and  
 CC inflammation; in ovulation it weakens the walls of the Graafian  
 CC follicle. It activates the urokinase-type plasminogen activator,  
 CC collagenases and several complement zymogens, such as C1 and C5.  
 CC It cleaves fibrin, fibrinogen, chromospondin, laminin and von  
 CC Willebrand factor.  
 CC -!- CATALYTIC ACTIVITY: Preferential cleavage: Lys-|-Xaa -> Arg-|-Xaa;  
 CC higher selectivity than trypsin. Converts fibrin into soluble  
 CC products.  
 CC -!- ENZYME REGULATION: Converted into plasmin by plasminogen

CC activators, both plasminogen and its activator being bound to  
CC fibrin. Cannot be activated with streptokinase.  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- MISCELLANEOUS: Plasmin is inactivated by alpha-2-antiplasmin  
CC immediately after dissociation from the clot.  
CC -1- SIMILARITY: Belongs to the peptidase S1 family. Plasminogen  
CC subfamily.  
CC -1- SIMILARITY: Contains 5 kringle domains.  
CC -1- SIMILARITY: Contains 1 PAN domain.  
CC -----  
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CC use by non-profit institutions as long as its content is in no way  
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CC or send an email to [license@sdb.ch](mailto:license@sdb.ch)).  
CC -----  
CC EMBL, U33171; AAC8717.1; -.  
CC PIR, I46260; I46260.  
CC HSSP, P00747; 1BU1.  
CC MEROPS, S01.233; -.  
CC InterPro: IPR000001; Kringle.  
CC InterPro: IPR003014; PAN.  
CC InterPro: IPR003609; Pan\_app.  
CC InterPro: IPR009003; Pept\_Ser\_Cys.  
CC InterPro: IPR001254; Peptidase\_S1.  
CC InterPro: IPR001314; Peptidase\_S1A.  
CC InterPro: IPR003966; Peptidase\_S1A\_pr.  
CC Pfam, PF00051; Kringle; 5.  
CC Pfam, PF00024; PAN; 1.  
CC Pfam, PF00089; Trypsin; 1.  
CC PIRSF, PIRSF001150; Plasmin; 1.  
CC PRINTS, PR00722; CHYMOTRYPSIN.  
CC PRINTS, PR00018; KRINGLE.  
CC PRINTS, PR01505; PROTHROMBIN.  
CC ProDom, PD000395; Kringle; 5.  
CC SMART, SM00130; KR; 5.  
CC SMART, SM00473; PAN AP; 1.  
CC SMART, SM00020; TYP\_SPC; 1.  
CC PROSITE, PS00021; KRINGLE\_1; 5.  
CC PROSITE, PS50070; KRINGLE\_2; 5.  
CC PROSITE, PS50048; PAN; 1.  
CC PROSITE, PS50240; TRYPSIN\_DOM; 1.  
CC PROSITE, PS00134; TRYPSIN\_HIS; 1.  
CC PROSITE, PS00135; TRYPSIN\_SER; 1.  
CC Blood coagulation, fibrinolysis; Glycoprotein; Hydrolase; Kringle;  
CC Plasma; Repeat; Serine protease; Signal; Tissue remodeling; Zymogen.  
CC FT SIGNAL 1 19 By similarity.  
CC FT CHAIN 20 810 Plasminogen.  
CC FT CHAIN 582 582 Plasmin heavy chain A (By similarity).  
CC FT CHAIN 583 810 Plasmin light chain B (By similarity).  
CC FT DOMAIN 20 98 PAN.  
CC FT DOMAIN 583 810 Serine protease.  
CC FT DOMAIN 103 181 Kringle 1.  
CC FT DOMAIN 185 262 Kringle 2.  
CC FT DOMAIN 275 352 Kringle 3.  
CC FT DOMAIN 379 456 Kringle 4.  
CC FT DOMAIN 482 561 Kringle 5.  
CC FT ACT\_SITE 622 622 Charge relay system.  
CC FT ACT\_SITE 665 665 Charge relay system.  
CC FT ACT\_SITE 760 760 Charge relay system.  
CC FT CAROHD 339 339 N-linked (GlcNAc...) (Potential).  
CC SEQUENCE 810 AA; 90902 MW; 8E75780946017A16 CRC64;  
Query Match 80.3%; Score 1237; DB 1; Length 810;  
Best Local Similarity 77.9%; Pred. No. 5,5e-86;  
Matches 201; Conservative 26; Mismatches 31; Indels 0; Gaps 0;  
QY 1 VYLSECKTGNGKNGYRGTMSTKNGITCQKMSSTSPHRRPSPATHPSEGLEENYCRNPDN 60  
DB 98 WYLSECKTGNGKNGYRGTMSTKNGITCQKMSSTSPHRRPSPATHPSEGLEENYCRNPDN 157

QY 61 DPQGPWCYTTDPKRYDYCDILECEBCHMGSENYDGKISKTMGSLGECQAMPDSPPH 120  
DB 158 DPKGPWCYTTDPKRYDYCDILECEBCHMGSENYDGKISKTMGSLGECQAMPDSPPH 217  
QY 121 GYIPSKFPNNKLNKKNCRNPDRELPMWCFTTDPNKMELCDIRCTTTPPSGPTVQCL 180  
DB 218 GFIPSKFPNNKLNKKNCRNPDRELPMWCFTTDPNKMELCDIRCTTTPPSGPTVQCL 277  
QY 181 GTGENYAGNVAIVYSGHLCQMSAOPHTERTPENPPCKNLDENYCRNPDGRAPMCHT 240  
DB 278 GNGEHYAGNVAIVYSGHLCQMSAOPHTERTPENPPCKNLDENYCRNPDGRAPMCHT 337  
QY 241 TNSQVREWCYCKIPSCDS 258  
DB 338 TNSQVREWCYCKIPSCDS 355  
RESULT 10  
QY 07TP84 PRELIMINARY; PRT; 759 AA.  
AC 07TP84;  
DT 01-OCT-2003 (TrEMBLrel. 25, Created)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Ab1-346.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Xu C.S., Li W.Q., Li Y.C., Yan H.M., Chang C.F., Zhao L.F., Ma H.,  
RA Yang L., Wang S.F., Han H.P., Wang G.P., Chai L.Q., Yuan J.Y.,  
RA Yang K.U., Shi J.B., Rahman S., Wang Q.N., Zhang J.B.,  
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL, AY325159; AAP92560.1; -.  
DR HSSP, P00747; 1BU1.  
DR GO, GO:0008233; F:peptidase activity; IEA.  
DR GO, GO:0004295; F:trypsin activity; IEA.  
DR GO, GO:0006508; P:proteolysis and peptidolysis; IEA.  
DR InterPro: IPR000001; Kringle.  
DR InterPro: IPR003014; PAN.  
DR InterPro: IPR001254; Peptidase\_S1.  
DR InterPro: IPR009003; Pept\_Ser\_Cys.  
DR InterPro: IPR001400; Somatotropin.  
DR Pfam, PF00051; Kringle; 5.  
DR Pfam, PF00024; PAN; 1.  
DR Pfam, PF00089; Trypsin; 2.  
DR ProDom, PD000395; Kringle; 5.  
DR SMART, SM00130; KR; 5.  
DR SMART, SM00020; TYP\_SPC; 1.  
DR PROSITE, PS00021; KRINGLE\_1; 5.  
DR PROSITE, PS50070; KRINGLE\_2; 5.  
DR PROSITE, PS00338; SOMATOTROPIN\_2; UNKNOWN\_1.  
DR PROSITE, PS50240; TRYPSIN\_DOM; 1.  
DR PROSITE, PS00134; TRYPSIN\_HIS; UNKNOWN\_1.  
KM Hydrolase; Kringle; Protease; Serine protease.  
SQ SEQUENCE 759 AA; 86056 MW; 1422BFA0C05C6DFA7 CRC64;  
Query Match 78.1%; Score 1203.5; DB 2; Length 759;  
Best Local Similarity 71.1%; Pred. No. 1,8e-83;  
Matches 204; Conservative 22; Mismatches 28; Indels 33; Gaps 2;  
QY 1 VYLSECKTGNGKNGYRGTMSTKNGITCQKMSSTSPHRRPSPATHPSEGLEENYCRNPDN 60  
DB 81 VYLSECKTGNGKNGYRGTMSTKNGITCQKMSSTSPHRRPSPATHPSEGLEENYCRNPDN 140  
QY 61 DPQGPWCYTTDPKRYDYCDILECEBCHMGSENYDGKISKTMGSLGECQAMPDSPPH 120  
DB 141 DPQGPWCYTTDPKRYDYCDILECEBCHMGSENYDGKISKTMGSLGECQAMPDSPPH 200  
QY 121 GYIPSKFPNNKLNKKNCRNPDRELPMWCFTTDPNKMELCDIRCTTTPPSGPTVQCL 166  
DB 121 GYIPSKFPNNKLNKKNCRNPDRELPMWCFTTDPNKMELCDIRCTTTPPSGPTVQCL 166

Db	201	GVIPAKPFSJKNLKNMYCRNPDBEPRMRCCTTDPNKRMEVCDIPRCTIVVIVIVIVITF	260
Qy	167	-----TPPSSGPTVQCLKGTGENTRGNVAVTVSGTCHQWSAQPTHTH	211
Db	261	IFIIIFIIIFIIIFIIIMFPLPLKSSLT-----GRGENYGVTSVTSAGTKCRWSBQFHRAN	316
Qy	212	RTPEHFPCKNLNDENYCRNPDGRAPWCHTNTNSQVREXKISCSDBS	258
Db	317	RTPEHFPCKNLNDENYCRNPDGETAPWCYTTDLSQRLMEYCEIPSCGSS	363
RESULT 11			
ID	PLMN	MACBU	STANDARD; PRT; 806 AA.
AC	O18783;		
DT	25-OCT-2004	(Rel. 45, Created)	
DT	25-OCT-2004	(Rel. 45, Last sequence update)	
DT	25-OCT-2004	(Rel. 45, Last annotation update)	
DE	Plasminogen	precursor (EC 3.4.21.7).	
GN	Name=PLG;		
OS	Macropus eugenii (Tamar wallaby).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OX	Mammalia; Metatheria; Diprotodontia; Macropodidae; Macropus.		
NCBI	TaxID=9315;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Liver;		
RX	MEDLINE=96004511; PubMed=9342350; DOI=10.1073/pnas.94.22.11992;		
RA	Lawn R.M., Schwartz K., Patchy L.;		
RT	"Convergent evolution of apolipoprotein(a) in primates and hedgehog";		
RL	Proc. Natl. Acad. Sci. U.S.A. 94:11992-11997(1997).		
CC	-1- FUNCTION: Plasmin dissolves the fibrin of blood clots and acts as		
CC	a proteolytic factor in a variety of other processes including		
CC	embryonic development, tissue remodeling, tumor invasion, and		
CC	inflammation; in ovulation it weakens the walls of the Graafian		
CC	follicle. It activates the urokinase-type plasminogen activator,		
CC	collagenases and several complement zymogens, such as C1 and C5.		
CC	It cleaves fibrin, fibronectin, thrombospondin, laminin and von		
CC	Willebrand factor. (By similarity).		
CC	-1- CATALYTIC ACTIVITY: Preferential cleavage: Lys- -Xaa > Arg- -Xaa;		
CC	higher selectivity than trypsin. Converts fibrin into soluble		
CC	products		
CC	-1- ENZYME REGULATION: Converted into plasmin by plasminogen		
CC	activators, both plasminogen and its activator being bound to		
CC	fibrin. Activated with catalytic amounts of streptokinase (By		
CC	similarity).		
CC	-1- SUBCELLULAR LOCATION: Secreted.		
CC	-1- MISCELLANEOUS: Plasmin is inactivated by alpha-2-antiplasmin		
CC	immediately after dissociation from the clot (By similarity).		
CC	-1- MISCELLANEOUS: In the presence of the inhibitor, the activation		
CC	involves only cleavage after Arg-576, resulting in 2 chains held		
CC	together by 2 disulfide bonds. Without the inhibitor, the		
CC	activation involves also removal of the activation peptide (By		
CC	similarity).		
CC	-1- SIMILARITY: Belongs to the peptidase S1 family. Plasminogen		
CC	subfamily.		
CC	-1- SIMILARITY: Contains 5 kringle domains.		
CC	-1- SIMILARITY: Contains 1 PAN domain.		
CC	-----		
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration		
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -		
CC	the European Bioinformatics Institute. There are no restrictions on its		
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CC	or send an email to <a href="mailto:license@isb-sb.ch">license@isb-sb.ch</a> ).		
CC	-----		
DR	EMBL; AF012297; AAB65760.1; -		
DR	HSSP; P00747; 1BUI.		
DR	MEROPS; S01.233. -		
DR	InterPro; IPR000001; Kringje.		
DR	InterPro; IPR003014; PAN.		
DR	InterPro; IPR003609; Pan app.		

QY	1	WTLS	SECT	GN	SK	YR	GTM	S	TK	NG	IT	OK	KS	SS	PH	RP	RS	PA	TH	PS	EG	LE	EN	CR	PD	N	60
DR	InterPro	IPR011358	Pept_S1A	Plasmin.																							
DR	InterPro	IPR009003	Pept_Ser_Cys.																								
DR	InterPro	IPR001254	Peptidase_S1.																								
DR	InterPro	IPR001314	Peptidase_S1A.																								
DR	InterPro	IPR003966	peptidase_S1A_pr.																								
DR	Pfam	PF00051	Kringle_5.																								
DR	Pfam	PF00024	PAN; 1.																								
DR	Pfam	PF00089	Trypsin; 1.																								
DR	PIRSEF	PIRSEF001150	Plasmin; 1.																								
DR	PRINTS	PRO0722	CHYMOTRYPSIN.																								
DR	PRINTS	PRO0018	KRINGLE.																								
DR	PRINTS	PRO1505	PROTHROMBIN.																								
DR	ProDom	PD000395	Kringle; 5.																								
DR	SMART	SMO0130	KR; 5.																								
DR	SMART	SMO0473	PAN_AP; 1.																								
DR	SMART	SMO0020	Tryp_Spc; 1.																								
DR	PROSITE	PS00021	KRINGLE_1; 5.																								
DR	PROSITE	PS50070	KRINGLE_2; 5.																								
DR	PROSITE	PS50948	PAN; 1.																								
DR	PROSITE	PS50240	TRYPSIN_DOM; 1.																								
DR	PROSITE	PS00134	TRYPSIN_HIS; 1.																								
DR	PROSITE	PS00135	TRYPSIN_SER; 1.																								
KW	Blood coagulation; Fibrinolysis; Glycoprotein; Hydrolyase; Kringle; Plasma; Repeat; Serine protease; Signal; Tissue remodeling; Zymogen.																										
FT	SIGNAL	1	19	Potential.																							
FT	CHAIN	20	806	Plasminogen.																							
FT	CHAIN	20	576	Plasmin heavy chain A (By similarity).																							
FT	PEPTIDE	20	96	Activation peptide (By similarity).																							
FT	CHAIN	97	576	Plasmin short form of chain A (By similarity).																							
FT	CHAIN	577	806	Plasmin light chain B (By similarity).																							

Db 98 IYLSDCSGNGRNVAGTILSKTSKITCQKMSDLSPHVENVYASKPPDAGLEKNTCRNPD 157  
Qy 61 DPGWGYTTTDBEKRYDYCDILECEECNHCSENGYDGIKSTWGLCQAMDSQSPHAF 120  
Db 158 DVKGWMTYTNNDINREYCDVECEDECHGCGENYRGITSTESIGICQWMDSEPHSH 217  
Qy 121 GYIPKFPKPKLKNKYCRNRPDELAPWCFTTDPNKRWELCDIPRCTTPSSGPTTYOCLK 180  
Db 218 EYIPKFPKPKLKNKYCRNRPDELAPWCFTTDPNKRWELCDIPRCTTPSSGPTTYOCLK 277  
Qy 181 GTGENYRGVAVTAVSGHTCOHWSAQTPHHRTSPNPKCNLDENYCNPPGKXAPWCHT 240  
Db 278 GCGENYRGVAVTAVSGHTCOHWSAQTPHHRTSPNPKCNLDENYCNPPGKXAPWCHT 337  
Qy 241 TNSQVREWCYKIPSCDSS 258  
Db 338 TNPDRQECYCAIPSCGTS 355  
RESULT 12  
Q6PBA6 PRELIMINARY; PRT; 818 AA.  
AC Q6PBA6;  
DT 05-JUL-2004 (TREMBlrel. 27, Created)  
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)  
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)  
DE Plasmidogen.  
GN Name=plg;  
OS Brachydanio rerio (Zebrafish) (Danio rerio).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
OC Cyprinidae; Danio.  
OX NCBI\_TaxID=7955;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Embryo;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,  
RA Alechul S.F., Zeeberg H., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan B., Moore T., Max S.I., Wang J., Heide F.,  
RA Ditchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stepleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usciti T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Rana S.S., Loguettano N.A., Peters G.J., Abramson R.D., Mulhany S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hilyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Rane J., Heaton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smallegange D.E., Scherch A., Schein J.E.,  
RA Jones S.J., Warr M.A.,  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences".  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Embryo;  
RX Strausberg R.,  
DT Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.  
DB EMBL; BC059801; AAH59801.1; -  
DR HSSP; P00747; 1B21.  
DR ZFIN; ZDB-GENE-030131-1411; plg.  
DR GO; GO:0005509; F:calcium ion binding; IEA.  
DR GO; GO:0004263; F:chymotrypsin activity; IEA.  
DR GO; GO:0008233; F:peptidase activity; IEA.  
DR GO; GO:0003809; F:thrombin activity; IEA.  
DR GO; GO:0004295; F:trypsin activity; IEA.  
DR GO; GO:0007596; P:blood coagulation; IEA.  
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.  
DR InterPro; IPR000001; Kringie.

DR InterPro; IPR003014; PAN.  
DR InterPro; IPR003609; Pan\_app.  
DR InterPro; IPR001254; Peptidase\_S1.  
DR InterPro; IPR001314; Peptidase\_S1A.  
DR InterPro; IPR003966; Peptidase\_S1A\_pr.  
DR InterPro; IPR009003; Pept\_Ser\_Cys.  
DR Pfam; PF00051; Kringie; 5.  
DR Pfam; PF00024; PAN; 1.  
DR Pfam; PF00089; Trypsin; 1.  
DR PRINTS; PR00722; CHYMOTRYPSIN.  
DR PRINTS; PR00018; KRINGLE.  
DR PRINTS; PR01505; PROTHROMBIN.  
DR PRODOM; PD000395; Kringie; 5.  
DR SMART; SM00130; KR; 5.  
DR SMART; SM00473; PAN AP; 1.  
DR SMART; SM00020; Tryp\_Spc; 1.  
DR PROSITE; PS00021; KRINGLE\_1; 3.  
DR PROSITE; PS50070; KRINGLE\_2; 5.  
DR PROSITE; PS50948; PAN; 1.  
DR PROSITE; PS50240; TRYPSIN\_DOM; 1.  
DR PROSITE; PS00134; TRYPSIN\_HIS; UNKNOWN\_1.  
DR PROSITE; PS00135; TRYPSIN\_SER; 1.  
DR HydroLase; Kringie; Protease; Serine protease.  
SQ SQUENCE 818 AA; 91635 MW; 55AC01BA38FF78 CRC64;  
Query Match 64.7%; Score 996; DB 2; Length 818;  
Best Local Similarity 61.2%; Pred. No. 1,3e-67;  
Matches 158; Conservative 34; Mismatches 66; Indels 0; Gaps 0;  
Qy 2 YISECTGNGKNGYRGITMSKTKNGITCQKMSSTSPHPRPSPATHPSEGLEENYCRNPD 61  
Db 106 YLLEFVNGIGMDYPRGKTSKTSKGTQRMWEGTFPHVNTITPAYPRADLESNFCRNPDD 165  
Qy 62 PGQWMTYTNNDINREYCDILECEECNHCSENGYDGIKSTWGLCQAMDSQSPHAF 121  
Db 166 KGGPWCYTTTDBEKRYDYCDILECEECNHCSENGYDGIKSTWGLCQAMDSQSPHAF 225  
Qy 122 YIYSKFPKPKLKNKYCRNRPDELAPWCFTTDPNKRWELCDIPRCTTPSSGPTTYOCLK 181  
Db 226 YLPSALPDKYLEENYCRNRPDELAPWCFTTDPNKRWELCDIPRCTTPSSGPTTYOCLK 285  
Qy 182 TGENYRGVAVTAVSGHTCOHWSAQTPHHRTSPNPKCNLDENYCNPPGKXAPWCHT 241  
Db 286 EGSYRGVAVTAVSGHTCOHWSAQTPHHRTSPNPKCNLDENYCNPPGKXAPWCHT 345  
Qy 242 NSQVREWCYKIPSCDSS 259  
Db 346 DPETREWCYCAIPSCGTS 363  
RESULT 13  
Q28398 PRELIMINARY; PRT; 2869 AA.  
AC Q28398;  
DT 01-NOV-1996 (TREMBlrel. 01, Created)  
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)  
DE Apolipoprotein(A) (Fragmen).  
OS Eritaceus europaeus (Western European hedgehog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Insectivora; Erinaceidae; Erinaceinae; Erinaceus.  
OX NCBI\_TaxID=9365;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Liver;  
RX MEDLINE=96025778; PubMed=7592597; DOI=10.1074/jbc.270.41.24004;  
RA Lamm R.M., Boommark N.W., Schwartz K., Lindahl G.E., Wade D.P.,  
RA Byrne C.D., Fong K.J., Meer K., Patsy L.,  
RT "The recurring evolution of lipoprotein(a). Insights from cloning of  
RT hedgehog apolipoprotein(a)".  
RL J. Biol. Chem. 270:24004-24009(1995).  
DB EMBL; U33170; AAC48522.1; -  
DR PIR; T18518; T18518.





OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;  
OC Xenopodinae; Xenopus.  
OX NCBI\_TaxID=8355;  
RN  
RP SEQUENCE FROM N.A.  
RA Ruiz i Altaba A., Thery C.;  
RL Submitted (MAY-1996) to the EMBL/Genbank/DDAJ databases.  
DR EMBL: U57455; AAB52574.1; -.  
DR HSP; P00746; IFDP.  
DR GO; GO:0005509; F:calcium ion binding; IEA.  
DR GO; GO:0004263; F:chymotrypsin activity; IEA.  
DR GO; GO:0008233; F:peptidase activity; IEA.  
DR GO; GO:0003809; F:thrombin activity; IEA.  
DR GO; GO:0004295; F:trypsin activity; IEA.  
DR GO; GO:0007596; P:blood coagulation; IEA.  
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.  
DR Pfam; PF00051; Kringle; 4.  
DR Pfam; PF00024; PAN; 1.  
DR Pfam; PF00089; Trypsin; 1.  
DR PIRSF; PIRSF001152; HGF\_MST1; 1.  
DR PRINTS; PR00722; CHYMOTRYPSIN.  
DR PRINTS; PR00018; KRINGLE.  
DR PRINTS; PR01505; PROTHROMBIN.  
DR ProDom; PD000395; Kringle; 4.  
DR SMART; SM00130; KR; 4.  
DR SMART; SM00473; PAN\_AP; 1.  
DR SMART; SM00020; TRY\_SP; 1.  
DR PROSITE; PS00021; KRINGLE\_1; 4.  
DR PROSITE; PS00070; KRINGLE\_2; 4.  
DR PROSITE; PS00948; PAN; 1.  
DR PROSITE; PS00240; TRYPSIN\_DOM; 1.  
KM Hydrolase; Kringle; Protease; Serine protease.  
SQ SEQUENCE 716 AA; 81971 MW; 508376A0E4398798 CRC64;

Query Match 52.6%; Score 809.5; DB 2; Length 716;  
Best Local Similarity 54.9%; Pred No. 1.8e-53;  
Matches 141; Conservative 28; Mismatches 83; Indels 5; Gaps 4;

OY 2 YLSCKTNGKNGKRYGTMSKTXNGITCQKMSSTSPHRRPSPATHPSSEGLEENYCRNPND 61  
Db 114 YIRDCVAGNGNTYRGTVSKTSGRTQGRWLKFPDHKFSPIHME--LEENYCRNPDS 171  
OY 62 PQGPWCYTTDEPKYDYCDILECEE-CMCSGENTYDGKISKTMGLECOAMDSQSPAH 120  
Db 172 PEGPWCYTTDKNIRHQYCGIKCEDAVCIATCNGEDYRGSVDRTEGKECCQMDLQTPAH 231  
OY 121 GYIPSKFPNKULKQYCNRPDLRLPWCFTTDPNRMWELCDIPRCTTPPPSS-GPTVQCL 179  
Db 232 PYKPEKYDLSLDNYCRNPDSSEHPWCYTTDPNVERKFCRIYCKCKORLSNIBITSTCF 291  
OY 180 KGTGENYRGNVAVTVSGHTCQWSAOTPHERTPENFPCKNLDENYCRNPDSGRAPCH 239  
Db 292 KERGGYRGKANTTSGIPQCRMSQTPQSHRFLPEKYPCKGIDENYCRNPDSSEAPWCF 351  
OY 240 TTNQVREYC-KIPSC 255  
Db 352 TTLPGMRMAYCFQIKRC 368

Search completed: July 27, 2005, 03:30:09  
Job time : 63 secs

log 1-3 + vactor